

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 00:41:05 ; Search time 8878.33 Seconds
(without alignments)
12582.818 Million cell updates/sec

Title: US-09-830-972-1
Perfect score: 3741
Sequence: 1 attgctcgtctctgggcggcg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Query Match	Length	DB	ID	
c	1	772.4	20.6	969	13	BU839934	BU839934 AGENCOURT
	2	767.2	20.5	785	14	CA511870	CA511870 UI-R-FJ0-
	3	753.4	20.1	842	13	BU709149	BU709149 UI-M-EW0-
	4	745	19.9	896	14	CB204418	CB204418 AGENCOURT
	5	725.6	19.4	796	14	CA504729	CA504729 UI-R-FJ0-
	6	709.8	19.0	805	12	BI730192	BI730192 603349739
	7	709.4	19.0	822	14	CB521332	CB521332 UI-M-GH0-
	8	707.8	18.9	986	13	BU841009	BU841009 AGENCOURT
	9	678.4	18.1	772	14	CF948588	CF948588 UI-M-HJ0-
	10	673.6	18.0	778	13	BU709106	BU709106 UI-M-EW0-
	11	662.6	17.7	777	14	CA320618	CA320618 UI-M-FW0-
	12	660.4	17.7	802	14	CA320635	CA320635 UI-M-FW0-
	13	659.2	17.6	951	13	BQ892001	BQ892001 AGENCOURT
	14	651.2	17.4	767	14	CF726835	CF726835 UI-M-HB0-
	15	648.6	17.3	739	13	BU612951	BU612951 UI-M-FR0-
	16	644.4	17.2	726	14	CF737320	CF737320 UI-M-HD0-
	17	638.4	17.1	724	14	CF729503	CF729503 UI-M-HD0-
	18	638.4	17.1	742	14	CA320833	CA320833 UI-M-FW0-
	19	638	17.1	638	14	CB576696	CB576696 AMGNNUC:C
	20	633.8	16.9	779	14	CB244702	CB244702 UI-M-FY0-
	21	633.4	16.9	862	9	AU079375	AU079375 AU079375
	22	617.6	16.5	688	14	CF540092	CF540092 UI-M-EX0-
	23	616	16.5	700	12	BI664179	BI664179 603289106
	24	608.2	16.3	935	13	BQ963057	BQ963057 AGENCOURT
	25	606.8	16.2	751	14	CA315995	CA315995 UI-M-FW0-
	26	605	16.2	673	14	CD349457	CD349457 UI-M-FY0-
	27	604.8	16.2	623	14	CB578453	CB578453 AMGNNUC:C
	28	604.8	16.2	691	13	BU707644	BU707644 UI-M-FR0-
	29	602	16.1	913	14	CB845105	CB845105 M2PN-0675
	30	598	16.0	609	14	CB580803	CB580803 AMGNNUC:N
	31	589.2	15.7	914	9	AU079162	AU079162 AU079162
	32	574.2	15.3	782	12	BI739239	BI739239 603359521
	33	570	15.2	810	12	BG668013	BG668013 DRABTB12
	34	568.6	15.2	698	13	BU058441	BU058441 UI-M-FO0-
	35	561	15.0	624	14	CB578355	CB578355 AMGNNUC:N
	36	561	15.0	646	9	AA791734	AA791734 vu08b07.r
	37	561	15.0	964	13	BQ900768	BQ900768 AGENCOURT
	38	560	15.0	681	14	CF742144	CF742144 UI-M-HB0-
	39	560	15.0	3533	11	AK034902	AK034902 Mus muscu
c	40	559.8	15.0	567	12	BI289826	BI289826 UI-R-DK0-
	41	556.8	14.9	717	13	BY756291	BY756291 BY756291
	42	556	14.9	556	14	CB613337	CB613337 AMGNNUC:N
	43	550.8	14.7	588	10	BF563033	BF563033 UI-R-B01-
	44	547.4	14.6	691	14	CB525239	CB525239 UI-M-FY0-
	45	546.8	14.6	817	14	CA322433	CA322433 UI-M-FX0-

ALIGNMENTS

RESULT 1
 BU839934
 LOCUS BU839934 969 bp mRNA linear EST 16-OCT-2002
 DEFINITION AGENCOURT_8947611 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6329890
 5', mRNA sequence.
 ACCESSION BU839934
 VERSION BU839934.1 GI:24024317
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 969)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
 Ph.D.
 cDNA Library Preparation: ResGen, Invitrogen Corp
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13783 row: g column: 11
 High quality sequence stop: 651.
 FEATURES Location/Qualifiers
 source 1. .969
 /organism="Mus musculus"
 /mol_type="mRNA"
 /db_xref="taxon:10090"
 /clone="IMAGE:6329890"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_130"
 /note="Organ: otocysts; Vector: pCMV-SPORT6.1; Site_1:
 EcoRV; Site_2: NotI; Cloned unidirectionally. Primer:
 Oligo dT. Average insert size 1.95 kb. Constructed by
 ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 20.6%; Score 772.4; DB 13; Length 969;
 Best Local Similarity 89.6%; Pred. No. 1.3e-103;
 Matches 878; Conservative 0; Mismatches 88; Indels 14; Gaps 4;

Qy 2172 CATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTT 2231
 ||||| ||||||||||||| | | || ||||||||| ||| |||||||||||||||||
 Db 1 CATGAGTGTAGCACTAAAACATCGGACTCAAAGGAAGAAATTAAAGAGCCTGAAAGTTT 60
 Qy 2232 TAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAA 2291
 ||||||||| ||||||| ||||||||||||||||||||| |||||||||||||

Db	61	TAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGCATGTGATTTAATTAA	120
Qy	2292	AGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTCTCTAATTATTTCAGAAATAGCAAA	2351
Db	121	AGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTATTTCAGAAATAGCAAA	180
Qy	2352	ATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGA	2411
Db	181	ATTTGAGAAGTCGGTGCCCTGATCACTGTGAGCTCGTGGATGATTCCTCACCCGAATCTGA	240
Qy	2412	ACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGC	2471
Db	241	ACCAGTTGACTTATTTAGTGATGATTCAATTCCTGAAGTCCCACAAACACAAGAGGAGGC	300
Qy	2472	TGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCCAGCACAAA--	2529
Db	301	TGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAACACAACACAAACA	360
Qy	2530	-GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCA	2588
Db	361	TAAGGAGAGACTTAGTGCCTCACCTCAGGAGGTAGGAAAGCCATATTTAGAGTCTTTTCA	420
Qy	2589	GCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTGACCAAAAA	2648
Db	421	GCCCAATTTACATATTACAAAAGATGCTGCATCTAATGAAATTCCAACATTGACCAAAAA	480
Qy	2649	GGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTT	2708
Db	481	GGAGACAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCCAATGATGACTT	540
Qy	2709	ACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTTCATCTCCGAT	2768
Db	541	ACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCAGATTTCATCTCCAT	600
Qy	2769	TGAGATAATAGATGAATTTCCACGTTTGTCTAGTGCTAAAGATGATTCTCCTAAATTAGC	2828
Db	601	TGAGATAATAGATGAGTTTCCACATTTGTCTAGTGCTANAGATGATTCTCCT-----	652
Qy	2829	CAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGG	2888
Db	653	-AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAGAGCGG	711
Qy	2889	GGCAGATTCAATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCC	2948
Db	712	NGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACATATCC	771
Qy	2949	TAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGC	3008
Db	772	TAAAGATGAAGCACATGTCTCAGATGAATTCT-CAAAAGTAGGTCCAGTGTATCTAAGGT	830
Qy	3009	ATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGT	3068
Db	831	GCCCCTATTGCTTCCCAATGGTTTCTGCTTGAATCTCAAATAG-AATGGGCCACATAGT	889
Qy	3069	TAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGA	3128
Db	890	TTAACCCAAAGTACTTACGGAAGAAGCAGAGGAAAAAACTTCCTTCTTGATCCGAGAAAGA	949

Qy 3129 GGACAGATCCCTGTCAGCTG 3148
 || ||||| |||||
 Db 950 GGGACGATCCCTGACAGCTG 969

RESULT 2
 CA511870

LOCUS CA511870 785 bp mRNA linear EST 15-NOV-2002

DEFINITION UI-R-FJ0-cpx-e-15-0-UI.r1 UI-R-FJ0 Rattus norvegicus cDNA clone
 UI-R-FJ0-cpx-e-15-0-UI 5', mRNA sequence.

ACCESSION CA511870

VERSION CA511870.1 GI:25002824

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 785)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics
 University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. James Lin, Universtiy of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research
 Genetics (www.resgen.com).

Seq primer: M13 REVERSE.

FEATURES

source

Location/Qualifiers

1. .785

/organism="Rattus norvegicus"

/mol_type="mRNA"

/strain="Sprague-Dawley"

/db_xref="taxon:10116"

/clone="UI-R-FJ0-cpx-e-15-0-UI"

/tissue_type="embryo"

/dev_stage="embryo"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-R-FJ0"

/note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;

UI-R-FJ0 is a cDNA library containing the following

tissue(s): rat embryo. The library was constructed

according to Bonaldo, Lennon and Soares, Genome Research,

6:791-806, 1996. First strand cDNA synthesis was primed

with an oligo-dT primer containing a Not I site. Double

stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CATCTCTACT. This library was created for the University of Iowa Program for Rat Gene Discovery and Mapping (Val Sheffield, Bento Soares and Tom Casavant)"

ORIGIN

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Query Match          20.5%;  Score 767.2;  DB 14;  Length 785;
Best Local Similarity 99.2%;  Pred. No. 7.7e-103;
Matches 780;  Conservative 0;  Mismatches 5;  Indels 1;  Gaps 1;

Qy      1699  ATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTTG TAGCAGTACAGGATTCT 1758
          |||
Db        1  ATAACAGAGAAGACTATCCCCACAACGTCAAATCCTTTCCTTG TAGCAGTACAGGATTCT 60

Qy      1759  GAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAAC 1818
          |||
Db        61  GAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAAC 120

Qy      1819  ATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAA 1878
          |||
Db       121  ATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAA 180

Qy      1879  GCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCT 1938
          |||
Db       181  GCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCT 240

Qy      1939  ATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCA 1998
          |||
Db       241  ATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCA 300

Qy      1999  ACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCA 2058
          |||
Db       301  ACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCA 360

Qy      2059  AGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTT 2118
          |||
Db       361  AGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTT 420

Qy      2119  AGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCCACCATATGAAGAAGCCATGAAT 2178
          |||
Db       421  AGTTATGACAGTATAAAGCTTGAGCCTGAAAATCCCCCACCATATGAAGAAGCCATGAAT 480

Qy      2179  GTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCA 2238
          |||
Db       481  GTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCA 540

Qy      2239  GCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACA 2298
          |||
Db       541  GCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACA 600

Qy      2299  AAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAG 2358
          |||

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Db      601 AAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTTCAGAAATAGCANAATTCGAG 660
Qy      2359 AAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTT 2418
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 AAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTT 720
Qy      2419 GACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATG 2478
        ||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db      721 GACTTATTTAGTGATGATTCGATTCCTGAAGT-CCACANACACAAGAGGAGGCTGTGATG 779
Qy      2479 CTCATG 2484
        |||||
Db      780 CTCATG 785

```

RESULT 3

BU709149

LOCUS BU709149 842 bp mRNA linear EST 15-JUL-2003

DEFINITION UI-M-EW0-caz-o-10-0-UI.r1 NIH_BMAP_EW0 Mus musculus cDNA clone
IMAGE:6419553 5', mRNA sequence.

ACCESSION BU709149

VERSION BU709149.1 GI:23642332

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 842)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .842

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:6419553"

/tissue_type="whole brain"

/dev_stage="embryo 15.5 dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_EW0"

/note="Organ: brain; Vector: pYX-Asc; Site_1: EcoR I;

Site_2: Not I; The library was constructed according to

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail, is GTGCGTGGAA. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

Query Match 20.1%; Score 753.4; DB 13; Length 842;
 Best Local Similarity 94.2%; Pred. No. 8.2e-101;
 Matches 792; Conservative 0; Mismatches 48; Indels 1; Gaps 1;

Qy	1677	AGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTT	1736
Db	2	AGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTT	61
Qy	1737	CCTTGTTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGT	1796
Db	62	CCTTGTTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAATTTATCAAAGGT	121
Qy	1797	GACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGC	1856
Db	122	GACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGTTCAGGAAGC	181
Qy	1857	ATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGGA	1916
Db	182	ATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGGA	241
Qy	1917	CTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCC	1976
Db	242	CTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTTTGCCC	301
Qy	1977	ATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGC	2036
Db	302	ATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGC	361
Qy	2037	ACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCC	2096
Db	362	GCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATCCCC	421
Qy	2097	ACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCC	2156
Db	422	ACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCCCCC	481
Qy	2157	ACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAA	2216
Db	482	ACCATATGAAGAAGCCATGAGTGTAGCACTAAAACATCGGACTCAAAGGAAGAAATTAA	541
Qy	2217	AGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGC	2276
Db	542	AGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGC	601

Qy 2277 GTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTA 2336
 |||
 Db 602 ATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTA 661
 Qy 2337 TTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTC 2396
 |||
 Db 662 TTCAGAAATAGCANAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTCGTGGATGATTC 721
 Qy 2397 CTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACA 2456
 |||
 Db 722 CTCACCCGAATCTGAACCAAGTTGACTTATTTAGTGATGATTCGAATTCCTGAAGT-CCACA 780
 Qy 2457 AACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGT 2516
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 Db 781 NACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGT 840
 Qy 2517 A 2517
 |
 Db 841 A 841

RESULT 4

CB204418

LOCUS CB204418 896 bp mRNA linear EST 05-FEB-2003

DEFINITION AGENCOURT_11276017 NIH_MGC_135 Mus musculus cDNA clone
 IMAGE:30138586 5', mRNA sequence.

ACCESSION CB204418

VERSION CB204418.1 GI:28241848

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 896)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: NDAM0041 row: k column: 11

High quality sequence stop: 686.

FEATURES

source

Location/Qualifiers

1. .896

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:30138586"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NIH_MGC_135"


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Db      604 GATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCATATTTGGAATCTGA 663

Qy      3405 AGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAA 3464
      ||||| ||||||||||||||||||||||| |||||||||||||||
Db      664 AGTTGCCATATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAA 723

Qy      3465 CAGCACAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAA 3524
      ||||||||||||| ||||| || |||||||||||||||||||
Db      724 CAGCACAATAAAAGAAATTGAGGCGTCTCTTCTTAGTTGATGATTTAGTTGATTCCCTGAA 783

Qy      3525 GTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCC-TTGTTC AATGGTCTGACAC 3583
      | ||||||||||||||| ||||||| ||||||| ||||||| |||||
Db      784 G-TTGCAGTGTTGATGTGGGTATTTACTTACGTTGGTGCCTTTGTTCAATGGTTTGACAC 842

Qy      3584 TACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCC 3620
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Db      843 TACTGATTTTAGCCCTGATCTCACTCTTCAGTATTCC 879

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RESULT 5

CA504729/c

LOCUS CA504729 796 bp mRNA linear EST 14-NOV-2002

DEFINITION UI-R-FJ0-cpx-e-15-0-UI.s1 UI-R-FJ0 Rattus norvegicus cDNA clone
UI-R-FJ0-cpx-e-15-0-UI 3', mRNA sequence.

ACCESSION CA504729

VERSION CA504729.1 GI:24995683

KEYWORDS EST.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 796)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Soares, MB

Coordinated Laboratory for Computational Genomics
University of Iowa

375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: bento-soares@uiowa.edu

Tissue Procurement: Dr. James Lin, Universtiy of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA
sequence: 1-35, >POLY_A#Simple_repeat (matched compliment)

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES
source

Location/Qualifiers

1. .796
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-FJ0-cpx-e-15-0-UI"
/tissue_type="embryo"
/dev_stage="embryo"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-R-FJ0"
/note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
UI-R-FJ0 is a cDNA library containing the following
tissue(s): rat embryo. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CATCTCTACT. This library
was created for the University of Iowa Program for Rat
Gene Discovery and Mapping (Val Sheffield, Bento Soares
and Tom Casavant)
TAG_TISSUE=rat-embryo
TAG_LIB=UI-R-FJ0
TAG_SEQ=CATCTCTACT"

ORIGIN

Query Match 19.4%; Score 725.6; DB 14; Length 796;
Best Local Similarity 99.3%; Pred. No. 9.9e-97;
Matches 728; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 952 TTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTTCATCCTCAGAAGGAACAATT 1011
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Db 733 TCTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTTCATCCTCAGAAGGAACAATT 674
|
Qy 1012 GAAGAAACTTTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTA 1071
|
Db 673 GAAGAACTNTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTA 614
|
Qy 1072 AATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAA 1131
|
Db 613 AATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAA 554
|
Qy 1132 GGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTG 1191
|
Db 553 GGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTG 494
|
Qy 1192 AGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCA 1251
|
Db 493 AGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCA 434
|
Qy 1252 CCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAA 1311
|

comprising
975-1163
99.3%

Db 433 CCTGTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAA 374
 Qy 1312 ATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAA 1371
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 Db 373 ATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAA 314
 Qy 1372 CAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT 1431
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 Db 313 CAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT 254
 Qy 1432 AATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTT 1491
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 Db 253 AATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTT 194
 Qy 1492 GGAAGGATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTG 1551
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 193 GGAAGGATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTG 134
 Qy 1552 AAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACC 1611
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 133 AAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACC 74
 Qy 1612 ACAGCAAACACTTTCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 1671
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 73 ACAGCAAACACTTTCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 14
 Qy 1672 AAAATAGAAGAAA 1684
 |||| | || ||
 Db 13 AAAAAAAAAAAAAA 1

RESULT 6

BI730192

LOCUS BI730192 805 bp mRNA linear EST 20-SEP-2001

DEFINITION 603349739F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5357385 5', mRNA sequence.

ACCESSION BI730192

VERSION BI730192.1 GI:15707205

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 805)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11908 row: n column: 10

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FEATURES
    source          Location/Qualifiers
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                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /db_xref="taxon:10090"
                    /clone="IMAGE:5357385"
                    /tissue_type="retina"
                    /lab_host="DH10B (phage-resistant)"
                    /clone_lib="NIH_MGC_94"
                    /note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
                    Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                    Average insert size 3.3 kb. Library enriched for
                    full-length clones and constructed by Life Technologies.
                    Note: this is a NIH MGC Library."
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Query Match 19.0%; Score 709.8; DB 12; Length 805;
Best Local Similarity 93.8%; Pred. No. 2.1e-94;
Matches 751; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

Qy	1854	AGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT	1913
Db	1	AGCATGTGAAAGTGAACTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGT	60
Qy	1914	GGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTG	1973
Db	61	GGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTTTG	120
Qy	1974	CCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGA	2033
Db	121	CCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGA	180
Qy	2034	AGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATC	2093
Db	181	AGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATC	240
Qy	2094	CCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCC	2153
Db	241	CCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCC	300
Qy	2154	CCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAAT	2213
Db	301	CCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAACATCGGACTCAAAGGAAGAAAT	360
Qy	2214	AAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCAT	2273
Db	361	TAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCAT	420
Qy	2274	TGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAA	2333
Db	421	TGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAA	480
Qy	2334	TTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGA	2393
Db	481	TTATTTCAGAAATAGCAAAATTTGAGAAGTCGGTGCTGATCACTGTGAGCTCGTGGATGA	540

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/dev stage="1, 5, and 15 days newborn"
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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_GH0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

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ORIGIN

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Query Match          19.0%;  Score 709.4;  DB 14;  Length 822;
Best Local Similarity 92.6%;  Pred. No. 2.4e-94;
Matches 771;  Conservative 0;  Mismatches 51;  Indels 11;  Gaps 2;

Qy      2762 CTCCGATTGAGATAAATAGATGAATTTCCACGTTTGTGTCAGTGCTAAAGATGATTCTCCTA 2821
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Db      1 CTCCCATTGAGATAAATAGATGAGTTTCCACATTGTGTCAGTGCTAAAGATGATTCTCCT- 59

Qy      2822 AATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCC 2881
      |||||||||||| |||||||||||| |||||||||||||||||||| |||
Db      60 -----AAGGAGTACACTGACCTAGAAAGTATCCAACAAAAGTGAAATTGCTAATGTCC 111

Qy      2882 AAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATA 2941
      | ||||||| ||| |||||||| ||||||||||||||||||||
Db      112 AGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATA 171

Qy      2942 TATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTAT 3001
      |||||||||||| |||||||| ||| ||||||||||||
Db      172 CATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTAT 231

Qy      3002 CTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCA 3061
      ||||| || ||| || | |||||| |||||||||||| ||| | ||||||||
Db      232 CTAAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCA 291

Qy      3062 GCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAG 3121
      ||||||||| ||||| |||||||||||||||||| ||||||||||||| ||||
Db      292 ACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAAACTTCCTTCTGATACAG 351

Qy      3122 AGAAAGAGGACAGATCCCTGTGAGCTGTATTGTGTCAGCAGAGCTGAGTAAACTTCAGTTG 3181
      |||||||||||||||| |||||||||||||||||| |||||||||||||
Db      352 AGAAAGAGGACAGATCCCTGACAGCTGTATTGTGTCAGCAGAGCTGAATAAACTTCAGTTG 411

Qy      3182 TTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTAT 3241
      ||||||||| |||||||||||||||||| |||||||||||||
Db      412 TTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTAT 471

Qy      3242 TCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTGTCAGTGTAACGGCCTACATTGCCTTGG 3301
      |||||||||||||||| |||||||||||||||||| |||||||||||||

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Db 472 TCCTGCTGCTGTCTCTGACAGTGTT--TCATTGTCAGTGTAACGGCCTACATTGCCTTGG 529
 Qy 3302 CCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGA 3361
 |||||
 Db 530 CCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAAGCTATCCAGA 589
 Qy 3362 AATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGG 3421
 |||||
 Db 590 AATCAGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCCATATCAGAGG 649
 Qy 3422 AATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAAC 3481
 |||||
 Db 650 AATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAAT 709
 Qy 3482 TGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGT 3541
 |||||
 Db 710 TGAGGCGTCTCTTCTTAGTTGATGACTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGT 769
 Qy 3542 GGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTA 3594
 |||||
 Db 770 GGGTATTTACTTACGTTGGTGCCTTGTTCAATGGTTTGACACTACTGACTTTA 822

RESULT 8

BU841009

LOCUS BU841009 986 bp mRNA linear EST 16-OCT-2002

DEFINITION AGENCOURT_10187690 NIH_MGC_134 Mus musculus cDNA clone

IMAGE:6518816 5', mRNA sequence.

ACCESSION BU841009

VERSION BU841009.1 GI:24025409

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 986)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe

cDNA Library Preparation: Invitrogen Corp

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM14101 row: c column: 09

High quality sequence start: 21

High quality sequence stop: 644.

FEATURES

source

Location/Qualifiers

1. .986

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:6518816"

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/tissue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_134"
/note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
Cloned unidirectionally. Primer: Oligo dT. Average insert
size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC Library."

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ORIGIN

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Query Match          18.9%;  Score 707.8;  DB 13;  Length 986;
Best Local Similarity 87.8%;  Pred. No. 4.1e-94;
Matches 832;  Conservative 0;  Mismatches 103;  Indels 13;  Gaps 5;

Qy      1728 AAATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTT 1787
        |||
Db      29 AAATCCTTTCCTTGTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAATTT 88

Qy      1788 ATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGT 1847
        |||
Db      89 ATCAAAGGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGT 148

Qy      1848 TCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAAC 1907
        |||
Db      149 TCAGGAAGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAAC 208

Qy      1908 AAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACA 1967
        |||
Db      209 AAAAGTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACA 268

Qy      1968 GCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGT 2027
        |||
Db      269 GCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGT 328

Qy      2028 TATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAG 2087
        |||
Db      329 TATGGAAGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAG 388

Qy      2088 TGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGA 2147
        |||
Db      389 TGCATCCCCACTAGAAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGA 448

Qy      2148 AAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGA 2207
        |||
Db      449 AAATCCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACGCAAAGGA 508

Qy      2208 AGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAACAGAAGCTCCTTATAT 2267
        |||
Db      509 AGAAATTAAAGAGCCTGANAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATAT 568

Qy      2268 ATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTT 2327
        |||
Db      569 ATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTT 628

Qy      2328 CTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGT 2387
        |||
Db      629 CTCTAATTATTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCCTGATCACTGTGAGCTCGT 688

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Qy	2388	GGAGGATTTCCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATTTCGATTCCCTGA	2447
Db	689	GGATGATTTCCTCACCCGAATCTGAACCAAGTTGACTTATTTAGTGATTCAATCCCTGA	748
Qy	2448	AGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC	2507
Db	749	AGTCCCACCAACACAAGAGGAAGCTGTGATGCTTATGAAAGAGAGTCTCACCTGAATGTC	808
Qy	2508	TGAGACAGTAGCCCAGC----ACAAAGAGGAGAGACTTAGTG----CCTCACCTCAGGAG	2559
Db	809	TGAGACAGTTACCCACCCCAACATAAGGGAGAGACTTAGTGCTTTCCCCTCCGGAGGGT	868
Qy	2560	CTAGGAAAGCCATATTTAGAGTCTTTT--CAGCCCAATTTACATAGT--ACAAAAGATGC	2615
Db	869	AGAAAAGGCCCTATTTTAGAGTCTTTTTCAGCCCAATTTACCTATTTACCAAAGGATGC	928
Qy	2616	TGCAT-CTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTCTT	2662
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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HJ0"
/note="Organ: Head; Vector: pYX-Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction ,ligated
with EcoR I adaptor , digested with NotI and then cloned
directionally into pYX-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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ORIGIN

```

Query Match          18.1%;  Score 678.4;  DB 14;  Length 772;
Best Local Similarity 92.8%;  Pred. No. 8.6e-90;
Matches 725;  Conservative 0;  Mismatches 47;  Indels 9;  Gaps 1;

Qy      2644 AAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGAT 2703
        |||
Db      1 AAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCCAATGAT 60

Qy      2704 GACTTACTTTCTTCTAAGGAAGACAAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCT 2763
        |||
Db      61 GACTTACTTTCTTCTAAGGAAGACAAAAATGAAAGAAAGTGAAACATTTTCAGATTCATCT 120

Qy      2764 CCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTAGTGCTAAAGATGATTCTCCTAAA 2823
        ||
Db      121 CCCATTGAGATAATAGATGAGTTTCCACATTTGTGCTAGTGCTAAAGATGATTCTCCT--- 177

Qy      2824 TTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAA 2883
        |||
Db      178 -----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAG 231

Qy      2884 AGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATA 2943
        |||
Db      232 AGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACA 291

Qy      2944 TATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCT 3003
        |||
Db      292 TATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTGTCT 351

Qy      3004 AAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGC 3063
        |||
Db      352 AAGGTGCCCTTATTGCTTCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCAAC 411

Qy      3064 ATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAG 3123
        |||
Db      412 ATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAAACTTCCTTCTGATACAGAG 471

Qy      3124 AAAGAGGACAGATCCCTGTGCTGCTGATTGTGCTAGCTGAGTAAAACTTCAGTTGTT 3183
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Db      472 AAAGAGGACAGATCCCTGTGCTGCTGATTGTGCTAGCTGAGTAAAACTTCAGTTGTT 531
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Qy	3184	GACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTC	3243
Db	532	GACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTC	591
Qy	3244	CTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG GCC	3303
Db	592	CTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG GCC	651
Qy	3304	CTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAA	3363
Db	652	CTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGGTGTGATCCANGCTATCCAGAAA	711
Qy	3364	TCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAA	3423
Db	712	TCAGATGAAGGCCACCCATTCAGGGCATATTTGGAATCTGAAGTTGGCATATCAGAGGAA	771
Qy	3424	T	3424
Db	772	T	772

BU709106

LOCUS	BU709106	778 bp	mRNA	linear	EST 15-JUL-2003
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DEFINITION UI-M-EW0-caz-g-18-0-UI.r1 NIH_BMAP_EW0 Mus musculus cDNA clone
IMAGE:6419369 5', mRNA sequence.

ACCESSION BU709106

VERSION BU709106.1 GI:23642247

KEYWORDS EST.

SOURCE *Mus musculus* (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 778)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin, Univeristy of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cdNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .778

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/organism="Mus musculus"
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/mol type="mRNA"
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/strain="C57BL/6"
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/db xref="taxon:10090"
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/clone="IMAGE:6419369"
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Qy	2233	AATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAA	2292
Db	482	AATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGCATGTGATTTAATTAAA	541
Qy	2293	GAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTAGCAAAATAGCAAAA	2352
Db	542	GAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTTCTCTAATTATTAGCAAAATAGCAAAA	601
Qy	2353	TTCGAGAAAGTCGGTGCCCGAACACGCTGAGCTAGTGAGGATTCCCTCACCTGAATCTGAA	2412
Db	602	TTTGAGAAAGTCGGTGCCCTGATCACTGTGAGCTCGTGATGATTCCCTCACCCGAATCTGAA	661
Qy	2413	CCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAAGTCCCACAAACACAAGAGGAGGCT	2472
Db	662	CCAGTTGACTTATTTAGTGATGATTCAATTCCCTGAAGT-CCACANACACAAGAGGAGGCT	720
Qy	2473	GTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTG	2509
Db	721	GTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTG	757

CA320618

LOCUS	CA320618	777 bp	mRNA	linear	EST 09-JUL-2003
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DEFINITION UI-M-FW0-ccb-k-24-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
IMAGE:6817393 5', mRNA sequence.

ACCESSION CA320618

VERSION CA320618.1 GI:24538742

KEYWORDS EST.

SOURCE *Mus musculus* (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 777)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES	Location/Qualifiers
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source      1. .777
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/organism="Mus musculus"
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/mol type="mRNA"
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/strain="C57BL/6"
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/db xref="taxon:10090"
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/clone="IMAGE:6817393"
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/tissue type="whole brain"
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Db      481 ATGAAATTCACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATA 540
Qy      2684 CTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTG 2743
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Db      541 CTGCAATTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTG 600
Qy      2744 AAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCTAGTG 2803
      ||| |||||
Db      601 AAACATTTTCGATTTCATCTCTCATTGAGATAATAGATGAGTTTCCCACATTGTCTAGTG 660
Qy      2804 CTAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAA 2863
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Db      661 CTAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAAA 711
Qy      2864 GTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTG 2923
      ||| |||||
Db      712 GTGAAATTGCTAATGTCCAGAGCGGNGGCAATTCGTTGCCTTGCTCAGAATTGCCCTGTG 771
Qy      2924 ACCTTT 2929
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Db      772 ACCTTT 777

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RESULT 12

CA320635

LOCUS CA320635 802 bp mRNA linear EST 09-JUL-2003

DEFINITION UI-M-FW0-ccb-o-24-0-UI.r1 NIH_BMAP_FW0 Mus musculus cDNA clone
IMAGE:6817489 5', mRNA sequence.

ACCESSION CA320635

VERSION CA320635.1 GI:24538759

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 802)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .802

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

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/clone="IMAGE:6817489"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_FW0"
/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

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ORIGIN

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Query Match          17.7%; Score 660.4; DB 14; Length 802;
Best Local Similarity 91.6%; Pred. No. 3.8e-87;
Matches 745; Conservative 0; Mismatches 54; Indels 14; Gaps 4;

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Qy      2148 AAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGA 2207
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Db       1 AAAATCCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACTCAAAGGA 60

Qy      2208 AGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATAT 2267
          || ||| ||||||||||||||||||||||||||||||||| ||||||| |||||||
Db       61 AGAAATTAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATAT 120

Qy      2268 ATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTT 2327
          ||||||| ||||||||||||||||||||||||||||||||||| ||||| |||
Db      121 ATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAGTT 180

Qy      2328 CTCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGT 2387
          ||||||| ||||||||||||||||||||||||||||||||| || ||| ||||| |||
Db      181 CTCTAATTATTTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCCTGATCACTGTGAGCTCGT 240

Qy      2388 GGAGGATTTCCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTTCGATTCCTGA 2447
          ||| ||||||||||| ||||||||||||||||||||||||||||||||| |||||||
Db      241 GGATGATTTCCTCACCCGAATCTGAACCAAGTTGACTTATTTAGTGATGATTCAATTCCTGA 300

Qy      2448 AGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC 2507
          ||||||| ||||||||||||||||||||||||||||||||| |||||||
Db      301 AGTCCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTC 360

Qy      2508 TGAGACAGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCCTCACCTCAGGAGCTAGG 2564
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Db      361 TGAGACAGTAACACAACACAACATAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTAGG 420

Qy      2565 AAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAA 2624
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Db	421	AAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCTAA	480
Qy	2625	TGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATAC	2684
Db	481	TGAAATTCCAACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATAC	540
Qy	2685	TGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGA	2744
Db	541	TGCAATTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGA	600
Qy	2745	AACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAAGTGC	2804
Db	601	AACATTTTCAGATTTCATCTCNCATTGAGATAATAGATGAGTTTCNCACATTTGTCAAGTGC	660
Qy	2805	TAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAG	2864
Db	661	TAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACACAAG	711
Qy	2865	TGAAATTGCTAATATCCAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGA	2924
Db	712	TGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGATTTG-CCTGTGA	770
Qy	2925	CCTTTCTTTCAAGAATATATATCCTAAAGATGA	2957
Db	771	CCTTTCTTTCAAG-ATACATATCCTAAAGATGA	802

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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6315079"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_129"
/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 2.2 kb. Constructed
by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
Library."

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ORIGIN

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Query Match          17.6%;  Score 659.2;  DB 13;  Length 951;
Best Local Similarity 89.3%;  Pred. No. 5.7e-87;
Matches 780;  Conservative 0;  Mismatches 79;  Indels 14;  Gaps 6;

Qy      2646 AAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGA 2705
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Db      11 AAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCCAATGATGA 70

Qy      2706 CTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCC 2765
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Db      71 CTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCAGATTCATCTCC 130

Qy      2766 GATTGAGATAATAGATGAATTTCCACGTTTGTGAGTGCTAAAGATGATTCTCCTAAATT 2825
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Db      131 CATTGAGATAATAGATGAGTTTCCACATTTGTGAGTGCTAAAGATGATTCTCCT----- 185

Qy      2826 AGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAG 2885
      ||| |
Db      186 ----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCTAATGTCCAGAG 241

Qy      2886 CGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATA 2945
      ||| |
Db      242 CGGGGCCAATTTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTCAAGAATACATA 301

Qy      2946 TCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAA 3005
      ||| |
Db      302 TCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCCAGTGTATCTAA 361

Qy      3006 GGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCAT 3065
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Db      362 GGTGCCCTTATTGCTTCAAATGTTTCTGCTTTGGAATCTCAAATAGAAATGGGCAACAT 421

Qy      3066 AGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAA 3125
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Db      422 AGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAAACTTCCTTCTGATACAGAGAA 481

Qy      3126 AGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTCAGTTGTTGA 3185
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Db      482 AGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAGCTGAATAAAACCTCAGTTGTTGA 541

Qy      3186 CCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCT 3245
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Db      542 CCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCT 601

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Qy 3246 GCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAAACGGCCTACATTG-CCTTGGCCC 3304
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 Db 602 GCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAAACGGCCTACATTGCCCTTGGCCC 661
 Qy 3305 TGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAAT 3364
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 Db 662 TGCTCTCTGTGACTATNCAGCTTAGGATATATAAGGGTGTGATCCAAGCTATCCAGAAAT 721
 Qy 3365 CAGATGAAGGCCA-CCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAA 3423
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 Db 722 CAGATGAAGGCCACCCCTTTTCAGGGCATATTTGGGATCTGAAGTTGCCATATCAGAAGAA 781
 Qy 3424 TTGG-TTCAGAAATACA-GTAATTCTGCTCTTGGTCATGTGAACAG-CACAATAAAAGAA 3480
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 Db 782 TTGGTTTCAGAAATATAGGAAATTCTGCTCTTGGGCATGGGGACCGCCACAATAAAAGAA 841
 Qy 3481 CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT 3513
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 Db 842 ATGGAGGGGTCTCCTCCTAAGTTAATGGATTT 874

RESULT 14

CF726835

LOCUS CF726835 767 bp mRNA linear EST 09-OCT-2003

DEFINITION UI-M-HB0-cki-m-06-0-UI.r1 NIH_BMAP_HB0 Mus musculus cDNA clone
 IMAGE:30548549 5', mRNA sequence.

ACCESSION CF726835

VERSION CF726835.1 GI:37601003

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 767)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

<http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .767

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6"

/db_xref="taxon:10090"

/clone="IMAGE:30548549"

/tissue_type="whole eye"

/dev_stage="embryo 12.5,13.5,14.5 dpc"

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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HB0"
/note="Organ: Eye; Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction ,ligated
with EcoR I adaptor , digested with NotI and then cloned
directionally into pYX-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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ORIGIN

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Query Match          17.4%;  Score 651.2;  DB 14;  Length 767;
Best Local Similarity 93.4%;  Pred. No. 8.5e-86;
Matches 718;  Conservative 0;  Mismatches 34;  Indels 17;  Gaps 3;

Qy      770 ATGAGACCCCTTTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCCTCCTCTGCAGAAA 829
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Qy      830 AAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCC 889
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Db      60 AAATTATGGATTTGAAGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCC 119

Qy      890 CATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTT 949
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Db      120 CATCTGTCCTGTTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTT 179

Qy      950 CTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTGCATCCTCAGAAGGAACAA 1009
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Db      180 CTTTTAAAGAACACGGATACCTTGGTAACTTATCAGCAGTGGCATCCACAGAAGGAACATA 239

Qy      1010 TTGAAGAAACTTTAAATGAAGCTTCTAAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTG 1069
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Db      240 TTGAAGAAACTTTAAATGAAGCTTCTAGAGAATTGCCAGAGAGGGCAACAAATCCATTTG 299

Qy      1070 TAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTA 1129
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Db      300 TAAATAGAGAGTCAGCAGAGTTTTTCAGTATTAGAATACTCAGAAATGGGATCATCTTTCA 359

Qy      1130 AAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTG 1189
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Db      360 ATGGCTCCCCAAAAGGAGAGTCAGCCATGTTAGTAGAAAACACTAAGGAAGAAGTAATTG 419

Qy      1190 TGAGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAAT 1249
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Db      420 TGAGGAGTAAAGACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCATAATCCACAAGAGT 479

Qy      1250 CACCT-----GTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAA 1294
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Db      480 CACCTGCGACCCTTACTAAAGTGGTTAAAGAAGACGGAGTTATGTCTCCAGAAAAGACAA 539
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Qy 1295 TGGACATTTTAAATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAG 1354
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 Db 540 TGGACATTTTAAATGAAATGAAAATGTCAGTGGTAGCACCTGTGAGGGAAGAGTATGCAG 599
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 Db 600 ATTTTAAGCCATTTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATG 659
 Qy 1415 TGCTGGCTGCTAGAGCTAATGTGGAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCC 1474
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 Db 660 TGCTGGCTGCTAGAGCTAATATGGAAAGTAAAGTGGACACAAAATGCTTGAAGATAGCC 719
 Qy 1475 TGGAGCAAAAAAGTCTTGGGAAGGATAGTGAAGGCAGAAATGAGGATGC 1523
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 Db 720 TGGAGC-NAAAGGTCATGGGAAGGATAGTGAAGGCAGAAATGAGAATGC 767

RESULT 15

BU612951

LOCUS BU612951 739 bp mRNA linear EST 20-FEB-2003

DEFINITION UI-M-FR0-cbd-a-04-0-UI.r1 NIH_BMAP_FR0 Mus musculus cDNA clone
 UI-M-FR0-cbd-a-04-0-UI 5', mRNA sequence.

ACCESSION BU612951

VERSION BU612951.1 GI:23279166

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 739)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@uiowa.edu

This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP)

Seq primer: pYX-5.

FEATURES

source

Location/Qualifiers

1. .739

/organism="Mus musculus"

/mol_type="mRNA"

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/clone="UI-M-FR0-cbd-a-04-0-UI"

/tissue_type="whole brain"

/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"

/lab_host="DH10B (T1 phage resistant)"

/clone_lib="NIH_BMAP_FR0"

/note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;

Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCGAGACAG. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN

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Query Match          17.3%;  Score 648.6;  DB 13;  Length 739;
Best Local Similarity 92.9%;  Pred. No. 2e-85;
Matches 694;  Conservative 0;  Mismatches 44;  Indels 9;  Gaps 1;

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Qy      3381 ATTCAGGGCATATTTAGAACTCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAG 3440
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Db      713 TAATTCTGCTCTTGGTCATGTGAACAG 739

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Job time : 8884.33 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 00:39:35 ; Search time 14076.4 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	3202.4	85.6	4627	10	AY102284	AY102284 Mus muscu
	4	3200.4	85.5	3821	10	AY114152	AY114152 Mus muscu
	5	3140.4	83.9	4518	10	BC056373	BC056373 Mus muscu
	6	2651	70.9	4063	10	AY102280	AY102280 Mus muscu
	7	2543.6	68.0	3815	10	BC032272	BC032272 Mus muscu
	8	2391.4	63.9	4166	9	AB040462	AB040462 Homo sapi
	9	2391.4	63.9	4789	9	AY102279	AY102279 Homo sapi
	10	2353.8	62.9	218532	2	AC131431	AC131431 Rattus no
	11	2353.8	62.9	238341	2	AC133315	AC133315 Rattus no
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	14	2343.6	62.6	4632	9	AF148537	AF148537 Homo sapi
	15	2333.2	62.4	4093	6	BD270070	BD270070 Secreted
	16	2323.8	62.1	4822	6	AR220865	AR220865 Sequence
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	22	2062	55.1	211357	2	AC113284	AC113284 Mus muscu
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	32	1769.4	47.3	2883	9	AF320999	AF320999 Homo sapi
	33	1541.2	41.2	1738	10	AB073672	AB073672 Mus muscu

	34	1486.6	39.7	2481	9	AF063601	AF063601 Homo sapi
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	38	1411.2	37.7	2386	6	AX099401	AX099401 Sequence
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	43	809.8	21.6	2782	6	AX700396	AX700396 Sequence
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ALIGNMENTS

RESULT 1

RNO242961

LOCUS RNO242961 4684 bp mRNA linear ROD 28-JAN-2000

DEFINITION Rattus norvegicus mRNA for Nogo-A protein.

ACCESSION AJ242961

VERSION AJ242961.1 GI:6822246

KEYWORDS Nogo-A protein.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1

AUTHORS Chen,M.S., Huber,A.B., van der Haar,M.E., Frank,M., Schnell,L.,
Spillmann,A.A., Christ,F. and Schwab,M.E.

TITLE Nogo-A is a myelin-associated neurite outgrowth inhibitor and an
antigen for monoclonal antibody IN-1

JOURNAL Nature 403 (6768), 434-439 (2000)

MEDLINE 20129258

PUBMED 10667796

REFERENCE 2 (bases 1 to 4684)

AUTHORS Van der Haar,M.E.

TITLE Direct Submission

JOURNAL Submitted (14-JUN-1999) Van der Haar M.E., Department of
Neuromorphology, Brain Research Institute, University of Zurich,
Winterthurerstrasse 190, Zurich, CH-8057, SWITZERLAND

FEATURES

Location/Qualifiers

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/mol_type="mRNA"
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gene

1. .4684
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CDS

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ORIGIN

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Query Match          100.0%;  Score 3739.4;  DB 10;  Length 4684;
Best Local Similarity 100.0%;  Pred. No. 0;
Matches 3740;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

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Db     61  ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT  120

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Db    121  CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA  180

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Db    241  GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC  300

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Db    301  CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG  360

Qy    361  GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG  420
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Db	661	CCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
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Db	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
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Qy	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Db	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Qy	901	CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
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Qy	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
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Db	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
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Db	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Qy	2641	ACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Db	2641	ACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Qy	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Db	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Qy	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTAGTGCTAAAGATGATTCTCCT	2820
Db	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTAGTGCTAAAGATGATTCTCCT	2820
Qy	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Db	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Qy	2881	CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Db	2881	CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Qy	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Db	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000

Qy	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
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Qy	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Db	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Qy	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT	3180
Db	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTT	3180
Qy	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Db	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Qy	3241	TTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Db	3241	TTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Qy	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Db	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Qy	3361	AAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Db	3361	AAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Qy	3421	GAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA	3480
Db	3421	GAATTGGTTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA	3480
Qy	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Db	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Qy	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG	3600
Db	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG	3600
Qy	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Db	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Qy	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Db	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Qy	3721	GGATTGAAGCGCAAAGCAGAT	3741
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RESULT 2
AX766046
LOCUS

AX766046

3489 bp

DNA

linear

PAT 25-JUN-2003

DEFINITION Sequence 1 from Patent WO03002602.
 ACCESSION AX766046
 VERSION AX766046.1 GI:32260128
 KEYWORDS .
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1
 AUTHORS Eisenbach-Schwartz,M. and Hauben,E.
 TITLE Nogo and nogo receptor derived peptides for t-cell mediated
 neuroprotection
 JOURNAL Patent: WO 03002602-A 1 09-JAN-2003;
 YEDA RESEARCH AND DEVELOPMENT Co. LTD. (IL)
 FEATURES Location/Qualifiers
 source 1. .3489
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 /mol_type="unassigned DNA"
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 exon 1. .3489
 ORIGIN

Query Match 93.3%; Score 3489; DB 6; Length 3489;
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 Matches 3489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	313	CCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG	372
Db	61	CCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG	120
Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	432
Db	121	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	180
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCCGCCGCGCTGCTGGAC	492
Db	181	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCCGCCGCGCTGCTGGAC	240
Qy	493	TTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCC	552
Db	241	TTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCC	300
Qy	553	GTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCTGCCG	612
Db	301	GTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCTGCCG	360
Qy	613	CCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCC	672
Db	361	CCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCC	420
Qy	673	CCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACG	732

Db	421	CCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACG	480
Qy	733	CCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCCTTTTGTCTTTCCT	792
Db	481	CCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCCTTTTGTCTTTCCT	540
Qy	793	GCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTGATGGAGCAG	852
Db	541	GCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTGATGGAGCAG	600
Qy	853	CCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCT	912
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Qy	913	GCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTT	972
Db	661	GCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTT	720
Qy	973	GGTAACTTATCAGCAGTGTCTATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCT	1032
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Qy	1033	TCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTT	1092
Db	781	TCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTT	840
Qy	1093	TCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCA	1152
Db	841	TCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCA	900
Qy	1153	GCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGAGGAT	1212
Db	901	GCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGAGGAT	960
Qy	1213	TTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGTAAAGAAGACAGA	1272
Db	961	TTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGTAAAGAAGACAGA	1020
Qy	1273	GTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTAGCA	1332
Db	1021	GTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTAGCA	1080
Qy	1333	CCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAAGAT	1392
Db	1081	CCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAAGAT	1140
Qy	1393	ACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAAAGTAAAGTGGAC	1452
Db	1141	ACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAAAGTAAAGTGGAC	1200
Qy	1453	AGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAGGATAGTGAAGGCAGA	1512
Db	1201	AGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAGGATAGTGAAGGCAGA	1260
Qy	1513	AATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGCTCCAGAGCATAT	1572
Db	1261	AATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGCTCCAGAGCATAT	1320

Qy	1573	ATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAACACTTTCCCTTTG	1632
Db	1321	ATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAACACTTTCCCTTTG	1380
Qy	1633	TTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAAGAAAGGAAGGCC	1692
Db	1381	TTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAAGAAAGGAAGGCC	1440
Qy	1693	CAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTTGTAGCAGTACAG	1752
Db	1441	CAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTTGTAGCAGTACAG	1500
Qy	1753	GATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTG	1812
Db	1501	GATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTG	1560
Qy	1813	TCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGT	1872
Db	1561	TCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGT	1620
Qy	1873	AATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCA	1932
Db	1621	AATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCA	1680
Qy	1933	GAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCT	1992
Db	1681	GAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCT	1740
Qy	1993	GAAGCAACTCCGTCACCAAGTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTC	2052
Db	1741	GAAGCAACTCCGTCACCAAGTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTC	1800
Qy	2053	CTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCT	2112
Db	1801	CTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCT	1860
Qy	2113	CCAGTTAGTTATGACAGTATAAAAGCTTGAGCCTGAAAACCCCCACCATATGAAGAAGCC	2172
Db	1861	CCAGTTAGTTATGACAGTATAAAAGCTTGAGCCTGAAAACCCCCACCATATGAAGAAGCC	1920
Qy	2173	ATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTT	2232
Db	1921	ATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTT	1980
Qy	2233	AATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAA	2292
Db	1981	AATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAA	2040
Qy	2293	GAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTTCAGAAATAGCAAAA	2352
Db	2041	GAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTTCAGAAATAGCAAAA	2100
Qy	2353	TTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCCTCACCTGAATCTGAA	2412
Db	2101	TTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCCCTCACCTGAATCTGAA	2160

Qy	2413	CCAGTTGACTTATTTAGTGATGATTCGATTCTGAAGTCCCACAAACACAAGAGGAGGCT	2472
Db	2161	CCAGTTGACTTATTTAGTGATGATTCGATTCTGAAGTCCCACAAACACAAGAGGAGGCT	2220
Qy	2473	GTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCCCAGCACAAAGAG	2532
Db	2221	GTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCCCAGCACAAAGAG	2280
Qy	2533	GAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCC	2592
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Qy	2593	AATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTGACCAAAAAGGAG	2652
Db	2341	AATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTGACCAAAAAGGAG	2400
Qy	2653	AAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTTACTT	2712
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Qy	2713	TCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCTCTCCGATTGAG	2772
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Qy	2773	ATAATAGATGAATTTCCACGTTTGTGCTGCTAAAGATGATTCTCCTAAATTAGCCAAG	2832
Db	2521	ATAATAGATGAATTTCCACGTTTGTGCTGCTAAAGATGATTCTCCTAAATTAGCCAAG	2580
Qy	2833	GAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCA	2892
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Db	2761	ATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAA	2820
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Qy	3253	TCTCTGACAGTGTTTCAGCATTGTGCTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCG	3312

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Db      3061 GTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAA 3120
Qy      3373 GGCCACCCATT CAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAG 3432
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Db      3121 GGCCACCCATT CAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAG 3180
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Db      3181 AAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTT 3240
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Db      3241 TTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACT 3300
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Qy      3673 AACAAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGC 3732
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RESULT 3

AY102284

LOCUS AY102284 4627 bp mRNA linear ROD 29-JAN-2003

DEFINITION Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.

ACCESSION AY102284

VERSION AY102284.1 GI:23379816

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4627)

AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.

TITLE Genomic Structure and Functional Characterisation of the Promoters
of Human and Mouse nogo/rtn4

JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)

MEDLINE 22376540

PUBMED 12488097

REFERENCE 2 (bases 1 to 4627)

AUTHORS Oertle,T. and Schwab,M.E.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057, Switzerland

REFERENCE 3 (bases 1 to 4627)

AUTHORS Van der Putten,H.

TITLE Direct Submission

JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma Inc., Basel, Switzerland

FEATURES Location/Qualifiers

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ORIGIN

Query Match 85.6%; Score 3202.4; DB 10; Length 4627;
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Db	136	CGGCTTGG-----TTCGGCCAGCCCGGCCCTCTGCCAGTCTTGCCCAACCCCCACA	185
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Qy	241	GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC	300
Db	245	GA-----CCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCGCGGATAGC	296
Qy	301	CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG	360
Db	297	CCGCCCCGGCCCCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG	356
Qy	361	GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG	420
Db	357	GACGAGGAAGACGAGGAG---GAGGAGGAGGACGACGAGGACCTGGAGGAATTGGAGGTG	413
Qy	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCG	480
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Qy	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCC	540
Db	471	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCC	530
Qy	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Db	531	GCGCCCCCACCGCCCCCTGAGAGGCAGCCGTCTTGGGAACGCAGCCCCGCGGCGTCCGCG	590
Qy	601	CCATCCCTGCCGCCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCAGAGGACGACGAGCCT	660
Db	591	CCATCCCTGCCGCCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCGGAGGACGACGAGCCT	650
Qy	661	CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
Db	651	CCAGCG-----CGGCCTCCGGCGCCAGCCGGCGCGAGCCCCCTAGCGGAGCCCGCCGCG	704
Qy	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Db	705	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCGGGCTCAGTGGATGAGACCCTT	764
Qy	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATAACCCTCCTCTGCAGAAAAAATTATGGAT	840
Db	765	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATAACCCTCCTCTGCAGAAAAAATTATGGAT	824
Qy	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900

Db 825 TTGAAGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCTCATCTGTCTCTG 884
 Qy 901 CTTGAAACTGCTGCCTCTCTTCCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA 960
 |||||
 Db 885 TTTGAAACTGCTGCCTCTCTTCCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA 944
 Qy 961 CATGGATACCTTGGTAACTTATCAGCAGTGTCTATCCTCAGAAGGAACAATTGAAGAACT 1020
 || |||||
 Db 945 CACGGATACCTTGGTAACTTATCAGCAGTGGCATCCACAGAAGGAACATTGAAGAACT 1004
 Qy 1021 TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGGCAACAAATCCATTTGTAAATAGAGAT 1080
 |||||
 Db 1005 TTAAATGAAGCTTCTAGAGAATTGCCAGAGAGGGGCAACAAATCCATTTGTAAATAGAGAG 1064
 Qy 1081 TTAGCAGAAATTTTCAGAAATAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA 1140
 | |||||
 Db 1065 TCAGCAGAGTTTTCAGTATTAGAATACTCAGAAATGGGATCATCTTTCAATGGCTCCCCA 1124
 Qy 1141 AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA 1200
 |||||
 Db 1125 AAAGGAGAGTCAGCCATGTTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA 1184
 Qy 1201 GACAAAGAGGATTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT----- 1254
 |||||
 Db 1185 GACAAAGAGGATTAGTTTGTAGTGCAGCCCTTCATAATCCACAAGAGTCACCTGCGACC 1244
 Qy 1255 -----GTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTT 1305
 |||||
 Db 1245 CTTACTAAAGTGGTTAAAGAAGACGGAGTTATGTCTCCAGAAAAGACAATGGACATTTTTT 1304
 Qy 1306 AATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCA 1365
 |||||
 Db 1305 AATGAAATGAAATGTCAGTGGTAGCACCTGTGAGGGAAGAGTATGCAGATTTAAGCCA 1364
 Qy 1366 TTTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCT 1425
 |||||
 Db 1365 TTTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCT 1424
 Qy 1426 AGAGCTAATGTGGAAAGTAAAGTGGACAGAAAATGCTTGGAAAGATAGCCTGGAGCAAAAA 1485
 |||||
 Db 1425 AGAGCTAATATGGAAAGTAAAGTGGACAAAAAATGCTTTGAAGATAGCCTGGAGCAAAAA 1484
 Qy 1486 AGTCTTGGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAA 1545
 |||||
 Db 1485 GGTCAATGGGAAGGATAGTGAAGGCAGAAATGAGAATGCTTCTTTCCCCAGGACCCAGAA 1544
 Qy 1546 CCTGTGAAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCCTTTACCTCAGCAACCGAA 1605
 | |||||
 Db 1545 CTTGTGAAGGACGGCTCCAGAGCGTACATCACCTGTGATTCCCTTTAGCTCAGCAACCGAG 1604
 Qy 1606 AGCACCACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAACAGAT 1665
 || |||||
 Db 1605 AGTACTGCAGCAAACATTTCCCTGTGCTAGAAGATCACACTTCAGAAAACAAAACAGAT 1664
 Qy 1666 GAAAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACG 1725
 |||||
 Db 1665 GAAAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACG 1724

Qy	1726	TCAAATCCTTTCCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACC	1785
Db	1725	TCAAATCCTTTCCCTTGTAGCAATACATGATTCTGAGGCAGATTATGTCACAACAGATAAT	1784
Qy	1786	TTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTA	1845
Db	1785	TTATCAAAGGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTA	1844
Qy	1846	G TTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAA	1905
Db	1845	G TTCAGGAAGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAA	1904
Qy	1906	ACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCA	1965
Db	1905	ACAAAAGTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCA	1964
Qy	1966	CAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATT	2025
Db	1965	CAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATT	2024
Qy	2026	GTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCC	2085
Db	2025	GTTATGGAAGCGCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCC	2084
Qy	2086	AGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCT	2145
Db	2085	AGTGCATCCCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCT	2144
Qy	2146	GAAAAACCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAG	2205
Db	2145	GAAAAACCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAACATCGGACTCAAAG	2204
Qy	2206	GAAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTAT	2265
Db	2205	GAAGAAATTAAAGAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTAT	2264
Qy	2266	ATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAT	2325
Db	2265	ATATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAG	2324
Qy	2326	TTCTCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTA	2385
Db	2325	TTCTCTAATTATTTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCTGATCACTGTGAGCTC	2384
Qy	2386	GTGGAGGATTTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCT	2445
Db	2385	GTGGATGATTTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTCAATTCCCT	2444
Qy	2446	GAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTG	2505
Db	2445	GAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTG	2504
Qy	2506	TCTGAGACAGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2505	TCTGAGACAGTAACACAACACAACATAAGGAGAGACTTAGTGCTTCACCTCAGGAGGTA	2564

Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCT	2622
Db	2565	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCT	2624
Qy	2623	AATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAAT	2682
Db	2625	AATGAAATTCCAACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAAT	2684
Qy	2683	ACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGT	2742
Db	2685	ACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGT	2744
Qy	2743	GAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCTAGT	2802
Db	2745	GAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAGTTTCCACATTTGTCTAGT	2804
Qy	2803	GCTAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAA	2862
Db	2805	GCTAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAA	2855
Qy	2863	AGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGT	2922
Db	2856	AGTGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGT	2915
Qy	2923	GACCTTTCTTTCAAGAAATATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCC	2982
Db	2916	GACCTTTCTTTCAAGAAATACATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCC	2975
Qy	2983	GAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAA	3042
Db	2976	AAAAGTAGGTCCAGTGTATCTAAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAA	3035
Qy	3043	CCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAA	3102
Db	3036	TCTCAAATAGAAATGGGCAACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAA	3095
Qy	3103	AAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAG	3162
Db	3096	AAACTTCCTTCTGATACAGAGAAAGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAG	3155
Qy	3163	CTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTG	3222
Db	3156	CTGAATAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTG	3215
Qy	3223	GTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTA	3282
Db	3216	GTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTA	3275
Qy	3283	ACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGC	3342
Db	3276	ACGGCCTACATTGCCTTGGCCCTGCTCTGTGACTATCAGCTTTAGGATATATAAGGGT	3335
Qy	3343	GTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCATATTTAGAATCT	3402
Db	3336	GTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCATATTTGGAATCT	3395
Qy	3403	GAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTG	3462

[illegible]

EDDLEDLEEVLERKPAAGLSAVPVPPAAAPLLDFSSDSVPPAPRGPLPAAPPTAPER
 QPSWERSPAASAPSLPPAAAVLP SKLPEDDEPPARPPAPAGASPLAEPAPPSTPAAP
 KRRGSGSVDETLFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFFETAAS
 LPSLSPLSTVVSFKEHGYLGNLSAVASTE GTIEETLNEASRELPERATNPFVNRESAEF
 SVLEYSEMGS SFNGSPKGESAMLVENTKEEVIVRSKDKEDLVCSAALHNPQESPATLT
 KVKEDGVMSPEKTMDIFNEMKMSVVAPVREEYADFKPFPEQAWEVKDTYEGSRDVLAA
 RANMESKVDKKCFEDSLEQKSHGKDSERNENASFPSTPELVKDGSRAYITCDSFTSA
 TESTAANIFPVLEDHTSENKTDEKKIEERKAQIITEKTS PKTSNPFLVAIH DSEADYV
 TTDNLSKVTEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQE
 SIYPTAQLCPSFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVPS
 YDGIKLEPENPPPYEEAMSVALKTS DAKEEIKEPESFNAAQEAEPYISIACDLIKE
 TKLSTEPSPGFSNYSEIAKFEKSVPDHCELVDDSSPESEPVDFLSDDSIPEVPQTQEE
 AVMLMKESL TEVSETVTQHKHKERLSASPQEVGKPYLESFQPNLHITKDAASNEIPTL
 TKKETISLQMEEFNTAIYSNDDLSSKEDKMESETFS DSSPIEIIDEFPTFVSAKDD
 SPKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDEAHVSD EFSKSRSS
 VSKVPLLLPNVSALESQIEMGNIVKPKVLTKEAEELKPSDTEKEDRSLTAVLSAELNK
 TSVVDLLYWRDIKKTGVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKG
 VIQAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVD
 SLKFAVLMWVFTYVGALENGLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKD
 AMAKIQA KIPGLKRKAE"

ORIGIN

Query Match 85.5%; Score 3200.4; DB 10; Length 3821;
 Best Local Similarity 92.8%; Pred. No. 0;
 Matches 3488; Conservative 0; Mismatches 211; Indels 61; Gaps 10;

Qy	2	TTGCTCGTCTGGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGA	61
Db	15	TTGCTCATCTGGGCGGCGGCGGCTGCTGCAACTGAGGACAGGACGGGTGGCGCATCTCGA	74
Qy	62	TCGCGAAGGCAGCAGAAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTC	121
Db	75	GCGCGGAGGCAGGAGGAGAAAGTCTTATTGTTCTGAGACTGTCGCCTTTGCGGGTTCTCTC	134
Qy	122	GGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCAACCCCCACAA	181
Db	135	GGCTTGG-----TTCGGCCAGCCCGGCTCTGCCAGTCTTGCCCAACCCCCACAA	184
Qy	182	CCGCCC GCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCG	241
Db	185	CCGCCC GCGGCTCTGAGGAGAAGTGGCCC-GCGGCGGCGAGTAGCTGCAGCATCATCGCCG	243
Qy	242	ACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCC	301
Db	244	A-----CCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCGCGGATAGCC	295
Qy	302	CGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCCGAGGACGAGGAGG	361
Db	296	CGCCCCGGCCCCCGCCGCTTTCAGTACCAGTTCGTGACGGAGCCCCGAGGACGAGGAGG	355
Qy	362	ACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAAGTGGAGGTGC	421
Db	356	ACGAGGAAGACGAGGAG---GAGGAGGAGGACGACGAGGACCTGGAGGAATTGGAGGTGC	412
Qy	422	TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCCCGCCGCCGCGC	481
Db	413	TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGTTCGGT---GCCCCCGCCGCCGCGC	469

Qy	482	CGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCG	541
Db	470	CGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCG	529
Qy	542	CGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGC	601
Db	530	CGCCCCCACCGCCCTGAGAGGCAGCCGTCCTGGGAACGCAGCCCCGCGGCGTCCGCGC	589
Qy	602	CATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCAGAGGACGACGAGCCTC	661
Db	590	CATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCGAGGACGACGAGCCTC	649
Qy	662	CGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCCGCCGCGC	721
Db	650	CAGCG-----CGGCCTCCGGCGCCAGCCGGCGCGAGCCCCCTAGCGGAGCCCCGCCGCGC	703
Qy	722	CCCCTTCCACGCCGCGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTT	781
Db	704	CCCCTTCCACGCCGCGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTT	763
Qy	782	TTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCTCCTCTGCAGAAAAAATTATGGATT	841
Db	764	TTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCTCCTCTGCAGAAAAAATTATGGATT	823
Qy	842	TGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCTTGC	901
Db	824	TGAAGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCTTGT	883
Qy	902	TTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAAC	961
Db	884	TTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAAC	943
Qy	962	ATGGATACCTTGGTAACTTATCAGCAGTGTATCCTCAGAAGGAACAATTGAAGAACTT	1021
Db	944	ACGGATACCTTGGTAACTTATCAGCAGTGGCATCCACAGAAGGAACATTGAAGAACTT	1003
Qy	1022	TAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATT	1081
Db	1004	TAAATGAAGCTTCTAGAGAAATTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAGT	1063
Qy	1082	TAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAA	1141
Db	1064	CAGCAGAGTTTTTCAGTATTAGAATACTCAGAAATGGGATCATCTTTCAATGGCTCCCCAA	1123
Qy	1142	AAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAG	1201
Db	1124	AAGGAGAGTCAGCCATGTTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAG	1183
Qy	1202	ACAAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----	1254
Db	1184	ACAAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCATAATCCACAAGAGTCACCTGCGACCC	1243
Qy	1255	-----GTGGGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTA	1306
Db	1244	TTACTAAAGTGTTAAAGAAGACGGAGTTATGTCTCCAGAAAAGACAATGGACATTTTTTA	1303

Qy	1307	ATGAAATGCAGATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCAT	1366
Db	1304	ATGAAATGAAAATGTCAGTGGTAGCACCTGTGAGGGAAGAGTATGCAGATTTTAAGCCAT	1363
Qy	1367	TTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTA	1426
Db	1364	TTGAACAAGCATGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTA	1423
Qy	1427	GAGCTAATGTGGAAAGTAAAGTGGACAGAAAAATGCTTGAAGATAGCCTGGAGCAAAAAA	1486
Db	1424	GAGCTAATATGGAAGTAAAGTGGACAAAAAATGCTTTGAAGATAGCCTGGAGCAAAAAA	1483
Qy	1487	GTCTTGGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAAGAAC	1546
Db	1484	GTCATGGGAAGGATAGTGAAGGCAGAAATGAGAATGCTTCTTTCCCCAGTACCCCAAGAAC	1543
Qy	1547	CTGTGAAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAA	1606
Db	1544	TTGTGAAGGACGGCTCCAGAGCGTACATCACCTGTGATTCTTTACCTCAGCAACCGAGA	1603
Qy	1607	GCACCACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATG	1666
Db	1604	GTACTGCAGCAAACATTTTCCCTGTGCTAGAAGATCACACTTCAGAAAATAAAACAGATG	1663
Qy	1667	AAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAACGT	1726
Db	1664	AAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAACGT	1723
Qy	1727	CAAAATCCTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCT	1786
Db	1724	CAAAATCCTTTCTTGTAGCAATACATGATTCCGAGGCAGATTATGTCACAACAGATAATT	1783
Qy	1787	TATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAG	1846
Db	1784	TATCAAAGGTGACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAG	1843
Qy	1847	TTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAA	1906
Db	1844	TTCAGGAAGCATGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAA	1903
Qy	1907	CAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCAC	1966
Db	1904	CAAAAGTGGACTTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCAC	1963
Qy	1967	AGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTG	2026
Db	1964	AGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTG	2023
Qy	2027	TTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCA	2086
Db	2024	TTATGGAAGCTCCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCA	2083
Qy	2087	GTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTG	2146
Db	2084	GTGCATCCCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTG	2143
Qy	2147	AAAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGG	2206

Db	2144	AAAATCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACGCAAAGG	2203
Qy	2207	AAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATA	2266
Db	2204	AAGAAATTAAAGAGCCTGAAAGTTTAAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATA	2263
Qy	2267	TATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATT	2326
Db	2264	TATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGGGT	2323
Qy	2327	TCTCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAG	2386
Db	2324	TCTCTAATTATTTCAGAAATAGCAAAATTTGAGAAGTCGGTACCTGATCACTGTGAGCTCG	2383
Qy	2387	TGGAGGATTCTCTACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTG	2446
Db	2384	TGGATGATTCTCTACCCGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTG	2443
Qy	2447	AAGTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGT	2506
Db	2444	AAGTCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGT	2503
Qy	2507	CTGAGACAGTAGCCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAG	2563
Db	2504	CTGAGACAGTAACACAACACAATAAGGAGAGACTTAGTGCCTCACCTCAGGAGGTAG	2563
Qy	2564	GAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTA	2623
Db	2564	GAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCTA	2623
Qy	2624	ATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATA	2683
Db	2624	ATGAAATTCCAACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATA	2683
Qy	2684	CTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTG	2743
Db	2684	CTGCAATTTATTCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTG	2743
Qy	2744	AAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAGTG	2803
Db	2744	AAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAGTTTCCACATTTGTCAGTG	2803
Qy	2804	CTAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAA	2863
Db	2804	CTAAAGATGATTCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAAA	2854
Qy	2864	GTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTG	2923
Db	2855	GTGAAATTGCTAATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTG	2914
Qy	2924	ACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCG	2983
Db	2915	ACCTTTCTTTCAAGAATACATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCA	2974
Qy	2984	AAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAAC	3043

KEYWORDS MGC.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 4518)
 AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
 Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
 Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
 Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
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 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
 TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 4518)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-2003) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Dr. Jim Lin, University of Iowa
 cDNA Library Preparation: M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
 Thomas L. Casavant.
 Web site: <http://genome.uiowa.edu>
 Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
 Bonaldo, M.F., Akabogu, I., Bair, T., Bair, J., Crouch, K., Davis, A.,
 Fishler, K., Keppel, C., Kucaba, T., Lebeck, M., Melo, A., Schaefer, K.,
 Scheetz, T., Smith, C., Snir, E., Tack, D., Trout, K., Walters, J.,
 Casavant, T., Soares, M.B.
 Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: Plate: Row: Column: 0.
 FEATURES Location/Qualifiers
 source 1. .4518
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RESULT 6

AY102280

LOCUS AY102280 4063 bp mRNA linear ROD 29-JAN-2003

DEFINITION Mus musculus RTN4 (Rtn4) mRNA, complete cds, alternatively spliced.

ACCESSION AY102280

VERSION AY102280.1 GI:23379808

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 4063)
 AUTHORS Oertle,T., Huber,C., van der Putten,H. and Schwab,M.E.
 TITLE Genomic Structure and Functional Characterisation of the Promoters
 of Human and Mouse nogo/rtn4
 JOURNAL J. Mol. Biol. 325 (2), 299-323 (2003)
 MEDLINE 22376540
 PUBMED 12488097

REFERENCE 2 (bases 1 to 4063)
 AUTHORS Oertle,T. and Schwab,M.E.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-2002) Brain Research Institute, University of
 Zurich and ETH Zurich, Winterthurerstr.190, Zuerich 8057,
 Switzerland

REFERENCE 3 (bases 1 to 4063)
 AUTHORS Van der Putten,H.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-2002) Nervous System Research, Novartis Pharma
 Inc., Basel, Switzerland

FEATURES Location/Qualifiers
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ORIGIN

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Qy	2013	TTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTC	2072
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Qy	2073	TGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTAT	2132
Db	1508	TGTAGCGCAGCCCAGTGCATCCCCACTAGAAGTACCGTCTCCAGTTAGTTATGACGGTAT	1567
Qy	2133	AAAGCTTGAGCCTGAAAAACCCCCACCATATGAAGAAGCCATGAATGTAGCACTAAAAGC	2192
Db	1568	AAAGCTTGAGCCTGAAAAATCCCCACCATATGAAGAAGCCATGAGTGTAGCACTAAAAAC	1627
Qy	2193	TTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAAC	2252
Db	1628	ATCGGACTCAAAGGAAGAAATTAAGAGCCTGAAAGTTTAAATGCAGCTGCTCAGGAAGC	1687
Qy	2253	AGAAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGA	2312
Db	1688	AGAAGCTCCTTATATATCCATTGCATGTGATTTAATTAAAGAAACAAAGCTCTCCACTGA	1747

Qy	2313	GCCAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGA	2372
Db	1748	GCCAAGTCCAGAGTTCTCTAATTATTCAGAAATAGCAAAATTTGAGAAGTCGGTGCCCTGA	1807
Qy	2373	ACACGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGA	2432
Db	1808	TCACGTGAGCTCGTGGATGATTCCTCACCCGAATCTGAACCAGTTGACTTATTTAGTGA	1867
Qy	2433	TGATTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAG	2492
Db	1868	TGATTCAATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAG	1927
Qy	2493	TCTCACTGAAGTGTCTGAGACAGTAGCCAGCACAAA---GAGGAGAGACTTAGTGCCTC	2549
Db	1928	TCTCACTGAAGTGTCTGAGACAGTAACACAACACAAACATAAGGAGAGACTTAGTGCCTC	1987
Qy	2550	ACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAA	2609
Db	1988	ACCTCAGGAGGTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATATTACAAA	2047
Qy	2610	AGATGCTGCATCTAATGACATTCCAACATTGACCAAAAAAGGAGAAAATTTCTTTGCAAAT	2669
Db	2048	AGATGCTGCATCTAATGAAATTCCAACATTGACCAAAAAAGGAGACAATTTCTTTGCAAAT	2107
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Qy	2730	AATAAAAGAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCC	2789
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Qy	2790	CACGTTTGTCAGTGCTAAAGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGA	2849
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 Qy 3510 AGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTT 3569
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 Db 3059 TGAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGCGTTAAGGA 3118
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 Db 3119 TGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3169

RESULT 7

BC032272

LOCUS BC032272 3815 bp mRNA linear ROD 16-APR-2003

DEFINITION Mus musculus reticulon 4, mRNA (cDNA clone IMAGE:5366860), partial cds.

ACCESSION BC032272

VERSION BC032272.1 GI:22749634

KEYWORDS .

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 3815)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
 Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
 Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
 Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
 Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
 Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
 McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
 Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
 Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
 Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S.,
 Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
 Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
 Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

TITLE Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
 MEDLINE 22388257
 PUBMED 12477932
 REFERENCE 2 (bases 1 to 3815)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: MGC help desk
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@nhgri.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 65 Row: f Column: 11
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis.

FEATURES Location/Qualifiers
 source 1. .3815
 /organism="Mus musculus"
 /mol_type="mRNA"

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Db	730	 GATTCCTTTTAGCTCAGCAACCGAGAGTACTGCAGCAAACATTTTCCCTGTGCTAGAAGAT	789
Qy	1642	CATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATA	1701
Db	790	 CACACTTCAGAAAACAAAACAGATGAAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATA	849
Qy	1702	ACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTTCCTTGTAGCAGTACAGGATTCTGAG	1761
Db	850	 ACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTTCCTTGTAGCAATACATGATTCTGAG	909
Qy	1762	GCAGATTATGTTACAACAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATG	1821
Db	910	 GCAGATTATGTCACAACAGATAATTTATCAAAGGTGACTGAGGCAGTAGTGGCAACCATG	969
Qy	1822	CCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCC	1881
Db	970	 CCTGAAGGTCTAACGCCAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGTGAACGAAGCC	1029
Qy	1882	ACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATA	1941
Db	1030	 ACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTGGTCCAGACATCAGAAGCTATA	1089
Qy	1942	CAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACT	2001
Db	1090	 CAAGAGTCAATTTACCCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACT	1149
Qy	2002	CCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGC	2061
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Qy	2062	GCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGT	2121
Db	1210	 ACTGGTGCTTCTGTAGCGCAGCCCAGTGCATCCCCACTAGAAGTACCGTCTCCAGTTAGT	1269
Qy	2122	TATGACAGTATAAAGCTTGAGCCTGAAAAACCCCCACCATATGAAGAAGCCATGAATGTA	2181
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Qy	2182	GCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCT	2241
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Db	1930	GATGAGTTTCCACATTTGTGCTAGTGCTAAAGATGATTCTCCT-----AAGGAGTAC	1980
Qy	2839	ACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCA	2898
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Qy	2899	TTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAA	2958
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Qy	2959	GTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCG	3018
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Qy	3019	CCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAA	3078
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Qy	3079	TCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCC	3138
Db	2221	GTACTTACGAAAGAAGCAGAGGAAAAAACTTCCTTCTGATACAGAGAAAGAGGACAGATCC	2280
Qy	3139	CTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGG	3198
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Qy	3319	ATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCAC	3378
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Qy	3439	AGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTA	3498
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Qy	3499	GTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTT	3558
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Qy	3679	AGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCA	3738
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Qy	3739	GA	3740
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RESULT 8

AB040462

LOCUS AB040462 4166 bp mRNA linear PRI 10-OCT-2001

DEFINITION Homo sapiens mRNA for RTN-XL, complete cds.

ACCESSION AB040462

VERSION AB040462.1 GI:11610574

KEYWORDS reticulon.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Tagami,S., Eguchi,Y., Kinoshita,M., Takeda,M. and Tsujimoto,Y.

TITLE A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on endoplasmic reticulum and reduces their anti-apoptotic activity

JOURNAL Oncogene 19 (50), 5736-5746 (2000)

MEDLINE 21010696

PUBMED 11126360

REFERENCE 2 (bases 1 to 4166)

AUTHORS Eguchi,Y., Tagami,S. and Tsujimoto,Y.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAR-2000) Yutaka Eguchi, Osaka University Graduate School of Medicine, Biomedical Research Center, Department of Medical Genetics; Yamadaoka 2-2, Suita, Osaka 567-0871, Japan (E-mail:eguchi@gene.med.osaka-u.ac.jp, Tel:+81-6-6879-3363, Fax:+81-6-6879-3369)

FEATURES Location/Qualifiers
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 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE"

ORIGIN

Query Match 63.9%; Score 2391.4; DB 9; Length 4166;
 Best Local Similarity 81.0%; Pred. No. 0;
 Matches 3100; Conservative 0; Mismatches 591; Indels 134; Gaps 22;

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ORIGIN

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Db	2215	ACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAAGAAAT	2274
Qy	2214	AAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAAGAAACAGAAGCTCCTTATATATCCAT	2273
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Qy	2274	TGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAA	2333
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Db	3055			
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Qy	3036	TTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGC	3095	
Db	3115			
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Qy	3096	AGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGCTGTATTGTC	3155	
Db	3175			
		TGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTC	3234	
Qy	3156	AGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGAC	3215	
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		AGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGAC	3294	
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RESULT 10

AC131431/c

LOCUS AC131431 218532 bp DNA linear HTG 19-NOV-2002

DEFINITION Rattus norvegicus clone CH230-256K14, WORKING DRAFT SEQUENCE.

ACCESSION AC131431

VERSION AC131431.3 GI:25084347

KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLLTOP.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 218532)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
 Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
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 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
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Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 218532)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (22-AUG-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 218532)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 19, 2002 this sequence version replaced gi:23101715.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GMSN
Center clone name: CH230-256K14
----- Summary Statistics

Assembly program: Phrap; version 0.990329
Consensus quality: 185268 bases at least Q40
Consensus quality: 186898 bases at least Q30
Consensus quality: 188068 bases at least Q20
Estimated insert size: 191844; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 1 218532: contig of 218532 bp in length.
FEATURES
 source Location/Qualifiers
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 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-256K14"
 misc_feature 1. .2141
 /note="wgs_contig"

ORIGIN

Query Match 62.9%; Score 2353.8; DB 2; Length 218532;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 2358; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Db 147688 CAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGG
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Qy 884 ATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAA 943
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Db 147628 ATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAA
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QY 3164 TGAGTAAACTTCAGTTGTTGACCT 3188
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RESULT 11
 AC133315

LOCUS AC133315 238341 bp DNA linear HTG 19-NOV-2002
 DEFINITION Rattus norvegicus clone CH230-525J22, WORKING DRAFT SEQUENCE, 2
 unordered pieces.

ACCESSION AC133315

VERSION AC133315.2 GI:25073594

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.

REFERENCE 1 (bases 1 to 238341)

AUTHORS Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
 Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
 Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
 Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
 Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
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 Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
 Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
 Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
 Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
 Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
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 Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
 Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
 Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
 Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
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 Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
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Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 238341)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 238341)
AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Nov 19, 2002 this sequence version replaced gi:22771260. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KAYT
Center clone name: CH230-525J22
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 219617 bases at least Q40
Consensus quality: 221191 bases at least Q30
Consensus quality: 222226 bases at least Q20
Estimated insert size: 224889; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 2 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 237118: contig of 237118 bp in length
 * 237119 237218: gap of unknown length
 * 237219 238341: contig of 1123 bp in length.

FEATURES Location/Qualifiers
 source 1. .238341
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 /clone="CH230-525J22"
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 /note="clone_boundary
 clone_end:T7
 site:
 end_sequence:BZ205043"
 misc_feature 24965. .25861
 /note="clone_boundary
 clone_end:Sp6
 site:
 end_sequence:BZ205045"

ORIGIN

Query Match 62.9%; Score 2353.8; DB 2; Length 238341;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 2358; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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 Db 126178 CAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGG
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 Qy 884 ATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAA 943
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 Db 126238 ATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAA
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 Qy 944 CTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAG 1003
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 Db 126298 CTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAG
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 Db 126418 CATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCAT
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RESULT 12

AX195249

LOCUS AX195249 4053 bp RNA linear PAT 28-AUG-2001

DEFINITION Sequence 5 from Patent WO0151520.

ACCESSION AX195249

VERSION AX195249.1 GI:15385809

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Strittmatter, S.M.

TITLE Nogo receptor-mediated blockade of axonal growth

JOURNAL Patent: WO 0151520-A 5 19-JUL-2001;

YALE UNIVERSITY (US)

FEATURES Location/Qualifiers

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/mol_type="unassigned RNA"

/db_xref="taxon:9606"

CDS 135. .3713

/note="unnamed protein product; Human mRNA for Nogo
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ORIGIN

Query Match 62.6%; Score 2343.6; DB 6; Length 4053;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

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Qy      194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
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Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
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Qy      433 CCCGCAGCCGGGCTGTCCGCAGTGCGGTGC-----CGCCCGCCCGCCCGCGCCGCTG 486
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Qy      598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
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Db      489 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 548

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
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Db      549 CCTCCGGCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 608

Qy      712 -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
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Db      609 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCGCCCAAGCGC 668

Qy      751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy      868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCCTCTCTTCCTTCT 927
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 Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA 1674
 Db 1563 ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA 1622
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Db	1683	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1742
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Db	1743	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1802
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Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
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Db	1983	GAAGCACCATTGAATTCTGCAGTTCTTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2042
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Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3390
Db	3300	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3359

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RESULT 13

AB020693

LOCUS AB020693 4053 bp mRNA linear PRI 16-JUN-1999

DEFINITION Homo sapiens mRNA for KIAA0886 protein, complete cds.

ACCESSION AB020693

VERSION AB020693.1 GI:4240260

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (sites)

AUTHORS Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirose,M.,
 Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

TITLE Prediction of the coding sequences of unidentified human genes.
 XII. The complete sequences of 100 new cDNA clones from brain which
 code for large proteins in vitro

JOURNAL DNA Res. 5 (6), 355-364 (1998)

MEDLINE 99156230

PUBMED 10048485

REFERENCE 2 (bases 1 to 4053)

AUTHORS Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.

TITLE Direct Submission

JOURNAL Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research Institute,
 Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
 Fax:+81-438-52-3914)

FEATURES

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ORIGIN

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Query Match      62.6%;  Score 2343.6;  DB 9;  Length 4053;
Best Local Similarity  81.3%;  Pred. No. 0;
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Qy      313  CCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG  372
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Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911
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Db 1803 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1862

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Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
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Db	2760	AGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2819

Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
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Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
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Db	3120	TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270
Db	3180	AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC	3239
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
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Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3390
Db	3300	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3359
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3360	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3419
Qy	3451	CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3420	CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA	3479
Qy	3511	GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3480	GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3539
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3540	AATGGTCTGACACTACTGATTTTGGCTCTCATTCACTCTTCAGTGTTTCTGTTATTTAT	3599
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3600	GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3659
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Db 3660 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3709

RESULT 14

AF148537

LOCUS AF148537 4632 bp mRNA linear PRI 09-SEP-2000

DEFINITION Homo sapiens reticulon 4a mRNA, complete cds.

ACCESSION AF148537

VERSION AF148537.1 GI:10039550

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4632)

AUTHORS Yang, J., Yu, L., Bi, A.D. and Zhao, S.Y.

TITLE Assignment of the human reticulon 4 gene (RTN4) to chromosome
2p14-->2p13 by radiation hybrid mapping

JOURNAL Cytogenet. Cell Genet. 88 (1-2), 101-102 (2000)

MEDLINE 20237542

PUBMED 10773680

REFERENCE 2 (bases 1 to 4632)

AUTHORS Zhou, Y., Yu, L. and Zhao, S.Y.

TITLE Direct Submission

JOURNAL Submitted (05-MAY-1999) Lab of Human Gene Research, Institute of
Genetics, Fudan University, No. 220 Handan Rd., Shanghai 200433,
P.R.China

FEATURES Location/Qualifiers

source

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polyA_signal
polyA_site
ORIGIN

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[illegible]

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Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
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Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
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Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
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Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
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Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
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Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
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Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
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Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
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Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
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Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1870	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1929
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1930	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1989
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGACGCCAGTGTA	2091
Db	1990	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2049
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2050	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2106
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2107	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAA	2166
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2167	GAAATTAAAGAGCCTGAAAAATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2226
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2227	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2286
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2287	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2346
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
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Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
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Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
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Db	3067	GAAGCTGAGAAAAAACTTCCTTCGGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3126
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Db	3127	TTTTCTAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3186
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Db	3187	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC	3246
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Db	2236	TCTATTGCATGTGATTTAATTAAGAAACAAAGCTTCTGCTGAACCAGCTCCGGATTTC	2295
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Db	2296	TCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2355
Qy	2389	GAGGATTCTCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCTGAA	2448
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Qy	2800	AGTGCTAAAGATGATTTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
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Db	2896	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2955
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2956	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	3015
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3016	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3075
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA	3150
Db	3076	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3135

Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3136	TTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3195
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270
Db	3196	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC	3255
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3256	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3315
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3390
Db	3316	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3375
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3376	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3435
Qy	3451	CTTGATTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3436	CTTGATTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA	3495
Qy	3511	GTTGATTCCCTGAAGTTTGCAAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3496	GTTGATTCTCTGAAGTTTGCAAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3555
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3556	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT	3615
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3616	GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3675
Qy	3691	GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740
Db	3676	GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA	3725

Search completed: September 11, 2004, 10:10:10
 Job time : 14092.4 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 10, 2004, 23:36:15 ; Search time 1309.89 Seconds
(without alignments)
12132.674 Million cell updates/sec

Title: US-09-830-972-1
Perfect score: 3741
Sequence: 1 attgctcgtctctggcgcgcg.....gattgaagcgcaaagcagat 3741

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	3739.4	100.0	4684	3	AAD01173	Aad01173 Rat neuri
2	3739.4	100.0	4684	6	ABN86600	Abn86600 Rat neuro
3	2343.6	62.6	4053	4	AAS09453	Aas09453 Human cDN
4	2343.6	62.6	4053	8	ACC81048	Acc81048 Human Nog
5	2343.6	62.6	4632	6	ABV94680	Abv94680 Human pan
6	2333.2	62.4	4093	3	AAA23454	Aaa23454 cDNA enco
7	2323.8	62.1	4822	6	ABS70449	Abs70449 Human bon

	8	2297.4	61.4	4698	7	ABX34563	Abx34563	Human	mdd
	9	2289.2	61.2	3579	3	AAZ56886	Aaz56886	Human	MAG
	10	2289.2	61.2	3579	4	AAF90324	Aaf90324	Human	NOG
	11	2289.2	61.2	3579	6	ABK90134	Abk90134	DNA	encod
	12	2289.2	61.2	3579	6	ABN86601	Abn86601	Human	neu
	13	1869.8	50.0	3833	3	AAD01174	Aad01174	Bovine	ne
	14	1411.2	37.7	2386	2	AAV30920	Aav30920	Human	sec
	15	1408	37.6	2386	5	AAF98399	Aaf98399	Human	cDN
	16	1088.8	29.1	1980	4	AAI98079	Aai98079	Human	neu
	17	809.8	21.6	2782	9	ADB85284	Adb85284	Rat	fooce
	18	564	15.1	1568	3	AAD01175	Aad01175	Rat	neuri
c	19	503.2	13.5	1758	4	AAF32725	Aaf32725	Human	sec
	20	498	13.3	2100	7	ABT42936	Abt42936	Human	neu
	21	497.4	13.3	600	4	AAF90323	Aaf90323	Human	NOG
	22	497.4	13.3	770	3	AAA72983	Aaa72983	Human	NSP
	23	497.4	13.3	799	2	AAV23695	Aav23695	Human	NSP
	24	497.4	13.3	1122	3	AAZ56888	Aaz56888	Human	MAG
	25	497.4	13.3	1122	4	AAF90325	Aaf90325	Human	NOG
	26	497.4	13.3	1213	2	AAX04379	Aax04379	Human	sec
	27	497.4	13.3	1216	6	ABA05903	Aba05903	Human	RTN
	28	497.4	13.3	2052	6	ABK90133	Abk90133	DNA	encod
	29	497.4	13.3	2235	6	ABV94681	Abv94681	Human	pan
	30	497.4	13.3	2240	3	AAC64406	Aac64406	Human	Nog
	31	495.8	13.3	991	2	AAX97587	Aax97587	Extended	
	32	495.8	13.3	1610	3	AAZ36230	Aaz36230	cDNA	enco
	33	495.8	13.3	1694	4	AAK94408	Aak94408	Human	ful
	34	483.6	12.9	868	3	AAZ56887	Aaz56887	Human	MAG
	35	475	12.7	1798	6	ABK90135	Abk90135	DNA	encod
	36	468	12.5	1514	6	ABK34580	Abk34580	Human	cDN
	37	391.6	10.5	1683	4	AAD08386	Aad08386	Human	sec
	38	375.6	10.0	422	7	ABX43312	Abx43312	Bovine	ES
	39	374	10.0	422	7	ABX46402	Abx46402	Bovine	ES
	40	323	8.6	460	2	AAV87027	Aav87027	EST	clone
	41	322.4	8.6	389	7	ABX39989	Abx39989	Bovine	ES
	42	316.2	8.5	615	4	AAK93939	Aak93939	Human	cDN
	43	302.6	8.1	423	7	ABX43927	Abx43927	Bovine	ES
	44	299	8.0	562	4	AAK93574	Aak93574	Human	cDN
c	45	278.8	7.5	742	4	AAI96236	Aai96236	Human	neu

ALIGNMENTS

RESULT 1

AAD01173

ID AAD01173 standard; cDNA; 4684 BP.

XX

AC AAD01173;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A cDNA.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; ss.
 XX
 OS Rattus sp.
 XX
 FH Key Location/Qualifiers
 FT CDS 253. .3744
 FT /*tag= a
 FT /product= "Nogo A"
 FT /transl_except= (pos:1462. .1464, aa:Ile)
 XX
 PN WO200031235-A2.
 XX
 PD 02-JUN-2000.
 XX
 PF 05-NOV-1999; 99WO-US026160.
 XX
 PR 06-NOV-1998; 98US-0107446P.
 XX
 PA (SCHW/) SCHWAB M E.
 PA (CHEN/) CHEN M S.
 XX
 PI Schwab ME, Chen MS;
 XX
 DR WPI; 2000-400052/34.
 DR P-PSDB; AAY71310.
 XX
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.
 XX
 PS Claim 26; Fig 2A; 122pp; English.
 XX
 CC The present sequence is a cDNA encoding rat Nogo A protein which is a
 CC potent neural cell growth inhibitor and is free of all central nervous
 CC system (CNS) myelin material with which it is natively associated. The
 CC present sequence was generated by fusing R018U37-3, R1-3U21 cDNA
 CC sequences isolated from hexanucleotides-primed rat brain stem/spinal cord
 CC library, and Olil8 cDNA from an oligo d(T)-primed rat oligodendrocyte
 CC library. Nogo proteins and fragments displaying neurite growth inhibitory
 CC activity are used in the treatment of neoplastic disease of the CNS e.g.
 CC glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
 CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
 CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
 CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
 CC promote Nogo activity can be used to treat or prevent hyperproliferative
 CC or benign dysproliferative disorders e.g. psoriasis and tissue
 CC hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to
 CC inhibit production of Nogo protein to induce regeneration of neurons or
 CC to promote structural plasticity of the CNS in disorders where neurite
 CC growth, regeneration or maintenance are deficient or desired. The animal
 CC models can be used in diagnostic and screening methods for predisposition
 CC to disorders and to screen for or test molecules which can treat or
 CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are
 CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the
 CC specification. However the specification does not include sequences for
 CC these SEQ ID numbers

SQ Sequence 4684 BP; 1358 A; 1048 C; 1112 G; 1166 T; 0 U; 0 Other;

Query Match 100.0%; Score 3739.4; DB 3; Length 4684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATTGCTCGTCTGGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG	60
Db	1	ATTGCTCGTCTGGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG	60
Qy	61	ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT	120
Db	61	ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT	120
Qy	121	CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA	180
Db	121	CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA	180
Qy	181	ACCGCCCGGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC	240
Db	181	ACCGCCCGGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC	240
Qy	241	GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC	300
Db	241	GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC	300
Qy	301	CCGCCCCGGCCTCCGCCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCAGGACGAGGAG	360
Db	301	CCGCCCCGGCCTCCGCCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCAGGACGAGGAG	360
Qy	361	GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACCTGGAGGTG	420
Db	361	GACGAGGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACCTGGAGGTG	420
Qy	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG	480
Db	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG	480
Qy	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC	540
Db	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC	540
Qy	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Db	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Qy	601	CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Db	601	CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Qy	661	CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCAGCCCCCTGGCGGAGCCCGCCGCG	720
Db	661	CCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCAGCCCCCTGGCGGAGCCCGCCGCG	720
Qy	721	CCCCCTTCCACGCCGGCCGCGCCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780

Db	721	CCCCCTTCCACGCCGCGCCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Qy	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT	840
Db	781	TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGAT	840
Qy	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Db	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Qy	901	CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Db	901	CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Qy	961	CATGGATACCTTGGTAACTTATCAGCAGTGTCACTCCTCAGAAGGAACAATTGAAGAACT	1020
Db	961	CATGGATACCTTGGTAACTTATCAGCAGTGTCACTCCTCAGAAGGAACAATTGAAGAACT	1020
Qy	1021	TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Db	1021	TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Qy	1081	TTAGCAGAATTTTCAGAATTAGAATATTAGAAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Db	1081	TTAGCAGAATTTTCAGAATTAGAATATTAGAAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Qy	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Db	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Qy	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Db	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Qy	1261	AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG	1320
Db	1261	AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG	1320
Qy	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Db	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Qy	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Db	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Qy	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAGGAT	1500
Db	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAGGAT	1500
Qy	1501	AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGACAGC	1560
Db	1501	AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGACAGC	1560
Qy	1561	TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
Db	1561	TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620

Qy	1621	ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAAATAAACAGATGAAAAAAAAATAGAA	1680
Db	1621	ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAAATAAACAGATGAAAAAAAAATAGAA	1680
Qy	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT	1740
Db	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT	1740
Qy	1741	GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Db	1741	GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Qy	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Db	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Qy	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Db	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Qy	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Db	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Qy	1981	TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCA	2040
Db	1981	TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATGGAAGCACCA	2040
Qy	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100
Db	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100
Qy	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Db	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Qy	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG	2220
Db	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAAGAG	2220
Qy	2221	CCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Db	2221	CCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Qy	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Db	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Qy	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Db	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Qy	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACA	2460
Db	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACA	2460

Qy	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Db	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Qy	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Db	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Qy	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Db	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Qy	2641	ACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Db	2641	ACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Qy	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Db	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Qy	2761	TCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCTAAAGATGATTCTCCT	2820
Db	2761	TCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTCAGTGCTAAAGATGATTCTCCT	2820
Qy	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Db	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Qy	2881	CAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Db	2881	CAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Qy	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Db	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Qy	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Db	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Qy	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Db	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Qy	3121	GAGAAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTTCAGTT	3180
Db	3121	GAGAAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAACCTTCAGTT	3180
Qy	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Db	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Qy	3241	TTCTGCTGCTGTCTCTGACAGTGTTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Db	3241	TTCTGCTGCTGTCTCTGACAGTGTTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Qy	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360

Db	3301		GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Qy	3361		AAATCAGATGAAGGCCACCCATTGAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Db	3361		AAATCAGATGAAGGCCACCCATTGAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Qy	3421		GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAA	3480
Db	3421		GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAA	3480
Qy	3481		CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Db	3481		CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Qy	3541		TGGGTGTTTACTTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTAGCTCTG	3600
Db	3541		TGGGTGTTTACTTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATTTTAGCTCTG	3600
Qy	3601		ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Db	3601		ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Qy	3661		CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Db	3661		CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Qy	3721		GGATTGAAGCGCAAAGCAGAT	3741
Db	3721		GGATTGAAGCGCAAAGCAGAT	3741

RESULT 2

ABN86600

ID ABN86600 standard; DNA; 4684 BP.

XX

AC ABN86600;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo encoding DNA.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;
 KW neurotransmitter receptor; rat; gene; ds.

XX

OS Rattus norvegicus.

XX

FH Key Location/Qualifiers

FT CDS 253. .3744

FT /*tag= a

FT /product= "Nogo-A"

XX

PN US2002072493-A1.

XX
PD 13-JUN-2002.
XX
PF 28-JUN-2001; 2001US-00893348.
XX
PR 19-MAY-1998; 98IL-00124500.
PR 21-JUL-1998; 98WO-US014715.
PR 22-DEC-1998; 98US-00218277.
PR 19-MAY-1999; 99US-00314161.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;
PI Moalem G;
XX
DR WPI; 2002-607255/65.
DR P-PSDB; ABB81074, ABB81076, ABB81077.
XX
PT Promoting nerve regeneration and preventing neuronal degeneration in the
PT central/peripheral nervous system from injury/disease, comprises
PT administering nervous system-specific activated T cells/antigen, or
PT analogs/peptides.
XX
PS Disclosure; Page 40-44; 93pp; English.
XX
CC The invention relates to promoting nerve regeneration or conferring
CC neuroprotection and preventing or inhibiting neuronal degeneration in the
CC central/peripheral nervous system (NS). The method involves administering
CC NS-specific activated T cells, NS-specific antigen, its analogue or its
CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or
CC combinations. The method is useful for promoting nerve regeneration and
CC preventing neuronal degeneration in central/peripheral nervous system
CC from injury/disease, where the injury is spinal cord injury, blunt
CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or
CC damages caused by surgery such as tumour excision. The disease is not an
CC autoimmune disease or neoplasm. The disease results in a degenerative
CC process occurring in either gray or white matter or both. The disease is
CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's
CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,
CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and
CC vitamin deficiency, intervertebral disc herniation, prion diseases such
CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral
CC neuropathies associated with various diseases, including but not limited
CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute
CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary
CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption
CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-
CC pathies, complications of various drugs (e.g., metronidazole) and toxins
CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia
CC telangiectasia, Friedreich's ataxia, amyloid polyneuropathies,
CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's
CC disease, or lipoproteinemia. The present sequence represents a DNA
CC encoding the rat neurotransmitter receptor protein Nogo (Nogo-A, Nogo-B
CC and Nogo-C), an example of NS-specific antigen
XX
SQ Sequence 4684 BP; 1358 A; 1047 C; 1112 G; 1167 T; 0 U; 0 Other;

Query Match 100.0%; Score 3739.4; DB 6; Length 4684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG	60
Db	1	ATTGCTCGTCTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCG	60
Qy	61	ATCGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT	120
Db	61	ATCGCGAAGGCAGGAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTT	120
Qy	121	CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA	180
Db	121	CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA	180
Qy	181	ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC	240
Db	181	ACCGCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC	240
Qy	241	GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC	300
Db	241	GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC	300
Qy	301	CCGCCCCGGCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG	360
Db	301	CCGCCCCGGCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG	360
Qy	361	GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG	420
Db	361	GACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTG	420
Qy	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG	480
Db	421	CTGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCG	480
Qy	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC	540
Db	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC	540
Qy	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Db	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
Qy	601	CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Db	601	CCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
Qy	661	CCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
Db	661	CCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCG	720
Qy	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Db	721	CCCCCTTCCACGCCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTT	780
Qy	781	TTTGCTCTTCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAATTATGGAT	840

Db	781	 TTTGCTCTTCCTGCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAATTATGGAT	840
Qy	841	TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Db	841	 TTGATGGAGCAGCCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTG	900
Qy	901	CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Db	901	 CTTGAAACTGCTGCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAA	960
Qy	961	CATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACT	1020
Db	961	 CATGGATACCTTGGTAACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACT	1020
Qy	1021	TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Db	1021	 TTAAATGAAGCTTCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAT	1080
Qy	1081	TTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Db	1081	 TTAGCAGAATTTTCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Qy	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Db	1141	 AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Qy	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Db	1201	 GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
Qy	1261	AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG	1320
Db	1261	 AAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATG	1320
Qy	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Db	1321	 TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Qy	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Db	1381	 GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
Qy	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAGGAT	1500
Db	1441	 AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAGGAT	1500
Qy	1501	AGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC	1560
Db	1501	 AGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC	1560
Qy	1561	TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
Db	1561	 TCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
Qy	1621	ACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAATAGAA	1680

Db	1621	ACTTTCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATAGAA	1680
Qy	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT	1740
Db	1681	GAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTCCTT	1740
Qy	1741	GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Db	1741	GTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTGACT	1800
Qy	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Db	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
Qy	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Db	1861	GAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGACTTG	1920
Qy	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Db	1921	GTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCATCA	1980
Qy	1981	TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGTTATGGAAGCACCA	2040
Db	1981	TTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGTTATGGAAGCACCA	2040
Qy	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100
Db	2041	TTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCACTG	2100
Qy	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Db	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCACCA	2160
Qy	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGAACAAAGGAAGGAATAAAAGAG	2220
Db	2161	TATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGAACAAAGGAAGGAATAAAAGAG	2220
Qy	2221	CCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Db	2221	CCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Qy	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Db	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Qy	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Db	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Qy	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACA	2460
Db	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAAGTCCCACAAACA	2460
Qy	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Db	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520

Qy	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Db	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATATTTAGAG	2580
Qy	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Db	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Qy	2641	ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTAATACTGCAATTTATTCAAAT	2700
Db	2641	ACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTAATACTGCAATTTATTCAAAT	2700
Qy	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Db	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Qy	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCTAGTGCTAAAGATGATTCTCCT	2820
Db	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCTAGTGCTAAAGATGATTCTCCT	2820
Qy	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Db	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Qy	2881	CAAAGCGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAAT	2940
Db	2881	CAAAGCGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAAT	2940
Qy	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Db	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Qy	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Db	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Qy	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAAGTTTCTTCTGACACA	3120
Db	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAAGTTTCTTCTGACACA	3120
Qy	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAAGTTTCTTCTGACACA	3180
Db	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAAGTTTCTTCTGACACA	3180
Qy	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Db	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Qy	3241	TTCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Db	3241	TTCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCCTTG	3300
Qy	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Db	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360

Qy	3361	AAATCAGATGAAGGCCACCCATT	CAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Db	3361	AAATCAGATGAAGGCCACCCATT	CAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Qy	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA		3480
Db	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAA		3480
Qy	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG		3540
Db	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG		3540
Qy	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG		3600
Db	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG		3600
Qy	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT		3660
Db	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT		3660
Qy	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT		3720
Db	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT		3720
Qy	3721	GGATTGAAGCGCAAAGCAGAT		3741
Db	3721	GGATTGAAGCGCAAAGCAGAT		3741

RESULT 3

AAS09453

ID AAS09453 standard; cDNA; 4053 BP.

XX

AC AAS09453;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human cDNA encoding the Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;

KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

KW demyelinating disease; multiple sclerosis; monophasis demyelination;

KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;

KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;

KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;

KW Canavan's disease; metachromatic leukodystrophy; viral infection;

KW Krabbe's disease; AB020693; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 135..3713

FT /*tag= a

FT /product= "Nogo protein"

XX

PN WO200151520-A2.

XX


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PD      19-JUL-2001.
XX
XX
PF      12-JAN-2001; 2001WO-US001041.
XX
XX
PR      12-JAN-2000; 2000US-0175707P.
PR      26-MAY-2000; 2000US-0207366P.
PR      29-SEP-2000; 2000US-0236378P.
XX
PA      (UYYA ) UNIV YALE.
XX
PI      Strittmatter SM;
XX
DR      WPI; 2001-442138/47.
DR      P-PSDB; AAU09453.
XX
XX
PT      Novel Nogo receptor protein useful for identifying modulator of Nogo
PT      protein or Nogo receptor protein, which is useful for treating central
PT      nervous system disorders.
XX
PS      Example 1; Page 95-100; 109pp; English.
XX
CC      The sequence (Genbank accession number AB0202693) encodes the human Nogo
CC      protein, a 250kDa myelin-associated axon growth inhibitor. The invention
CC      relates to the use of the nogo receptor, nogo protein, their nucleic
CC      acids, vectors expressing them and antibodies against them, to isolate
CC      agents which block nogo receptor mediated axonal growth. The agent is
CC      useful for treating a central nervous system disorder which is a result
CC      of cranial or cerebral trauma, spinal cord injury, stroke or a
CC      demyelinating disease selected from multiple sclerosis, monophasis
CC      demyelination, encephalomyelitis, multifocal leukoencephalopathy,
CC      panencephalitis, Marchiafava-Bignami disease, pontine myelinolysis,
CC      adrenoleukodystrophy, Pelizaeus-Merzbacher disease, Spongy degeneration,
CC      Alexander's disease, Canavan's disease, metachromatic leukodystrophy,
CC      viral infection and Krabbe's disease
XX
SQ      Sequence 4053 BP; 1189 A; 922 C; 922 G; 1020 T; 0 U; 0 Other;

Query Match          62.6%; Score 2343.6; DB 4; Length 4053;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

Qy      134 CACGACTCGGCCTGCCTGGCCCCTGCCAGTCTTGCCCCAACCCCCACAACCGCCCGCGACT 193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      16 CTCGGCTCAGTCGGCCAGCCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 75

Qy      194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      76 CTGAGACGCGGCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 134

Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGGCCT 312
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCTCGGACAGCCACCCCGGGCCG 191

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 CAGCCCGCGGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

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Qy	373	GAGGAGGACGAGGAGGAGGACGAGGACCTAGAGGAACCTGGAGGTGCTGGAGAGGAAG	432
Db	249	GAGGAGGAAGAGGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	308
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCCGCCGCCGCCGCCGCTG	486
Db	309	CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCCGCGCGCCCTG	368
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	369	ATGGACTTCGGAATGACTTCGTGCCGCCGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	428
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	429	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC	488
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	489	GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTGCCCTCCAAGCTCCCTGAGGACGACGAG	548
Qy	658	CCTCCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	549	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	608
Qy	712	-----CCCCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	609	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCCGCGCCCAAGCGC	668
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCCTTTTGTCTCTTCCTGCTGCATCTGAGCCT	807
Db	669	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCCTTTTGTCTCTTCCTGCTGCATCTGAGCCT	728
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCCTCTCTTCCTTCT	927
Db	786	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCTTCTCTTCCTTCT	845
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCA	987
Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	905
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	906	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	965
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	966	GAGAAGGCAAAAACCTTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1025
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1026	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1085
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224

Db	1086	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1145
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATGTCAGTAGTA	1329
Db	1206	GAAGTTGTGTCTTCAGAAAAGCAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGAA	1265
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1266	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1325
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1326	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1382
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG	1497
Db	1383	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATAATCACGAAAA	1442
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGAC	1557
Db	1443	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAGGTATAAAGGAT	1502
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614
Db	1503	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1562
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA	1674
Db	1563	ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA	1622
Qy	1675	ATAGAAGAAAGGAAGGCCAAATTATAACAGAGAAG---ACTAGCCCCAAACGTCAAAT	1731
Db	1623	ATAGAAGAAAAGAAGGCCCAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC	1682
Qy	1732	CCTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1683	CCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1742
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTAC	1851
Db	1743	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1802
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1803	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1862
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1863	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1922
Qy	1972	TGCCCATCATTTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031

Db	1923	TGCCCATCATTTGAAGAGT	CAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1982
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA		2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA		2042
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC		2151
Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC		2099
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA		2208
Db	2100	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA		2159
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA		2268
Db	2160	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA		2219
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC		2328
Db	2220	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTCTGCTGAACCAGCTCCGGATTTTC		2279
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG		2388
Db	2280	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT		2339
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCTTGAA		2448
Db	2340	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC		2399
Qy	2449	GTCCCACAAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A		2502
Db	2400	GTTCCACAAAACACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA		2459
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA		2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA		2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA		2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA		2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT		2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC		2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA		2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA		2699
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC		2799
Db	2700	ACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC		2759
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC		2856
Db	2760	AGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC		2819

Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACAGAATTG	2879
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2880	CCCCATGACCTTTCTTTGAAGAACATAACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2939
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3120	TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCA	3270
Db	3180	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCACTGACAGTATTCAGC	3239
Qy	3271	ATTGTGAGTGAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3240	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3299
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3390
Db	3300	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3359
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAAGAAATACAGTAATTCTGCT	3450
Db	3360	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGTACAGTAATTCTGCT	3419
Qy	3451	CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3420	CTTGGTCATGTGAAGTGCACGATAAAGGAAGTCAAGGCGCCTCTTCTTAGTTGATGATTTA	3479
Qy	3511	GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3480	GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3539
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3540	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTTATTTAT	3599
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3600	GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3659

QY 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
 || ||||| |||||||||||||||||||||||||||||||||||| ||
 Db 3660 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3709

RESULT 4

ACC81048

ID ACC81048 standard; cDNA; 4053 BP.

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AC ACC81048;

XX

DT 22-JUL-2003 (first entry)

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DE Human NogoA gene.

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KW Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis; gene;
 KW ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 135..3713

FT /*tag= a

FT /product= "Human NogoA"

XX

PN WO2003031462-A2.

XX

PD 17-APR-2003.

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PF 04-OCT-2002; 2002WO-US032007.

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PR 06-OCT-2001; 2001US-00972599.

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PA (UYYA) UNIV YALE.

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PI Strittmatter SM;

XX

DR WPI; 2003-393433/37.

DR P-PSDB; ABR59667.

XX

PT New human Nogo receptor polypeptides and nucleic acids, useful for
 PT decreasing inhibition of axonal growth by a central nervous system
 PT neuron, or in treating central nervous system disease, disorder or
 PT injury, e.g. spinal cord injury.

XX

PS Disclosure; Page 126-131; 148pp; English.

XX

CC The invention relates to a novel nucleic acid encoding a polypeptide
 CC comprising amino acid residues 27-309 of a 473 amino acid sequence (P1,
 CC human Nogo receptor (NgR) NTLRRCT domain), or residues 27-309 of P1 with
 CC 1-20 conservative amino acid substitutions, and less than a complete CTS
 CC domain, provided that a partial CTS domain, if present, consists of no
 CC more than the first 39 consecutive residues. The nucleic acid of the

Db 549 CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 608
 Qy 712 -----CCCCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
 Db 609 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC 668
 Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
 Db 669 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 728
 Qy 808 GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
 Db 729 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 785
 Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCCTCTCTTCCTTCT 927
 Db 786 TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCTTCTCTTCCTTCT 845
 Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGCTAACTTATCAGCA 987
 Db 846 CTGTCTCCTCTCTCAGCCGCTTCTTCAAAGAACATGAATACCTTGCTAATTTGTCAACA 905
 Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
 Db 906 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 965
 Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107
 Db 966 GAGAAGGCAAAAACCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 1025
 Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167
 Db 1026 TCAGAAATGGGATCATCGTTTCAAGGCTCTTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1085
 Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
 Db 1086 AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1145
 Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269
 Db 1146 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1205
 Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTAATGAAATGCAGATGTCAGTAGTA 1329
 Db 1206 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAA 1265
 Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389
 Db 1266 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1325
 Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437
 Db 1326 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1382
 Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497
 Db 1383 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA 1442

Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGAC 1557
 ||||| | || |||| | || ||||| ||||| ||||| | |||||
 Db 1443 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1502

Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA 1614
 | || ||||| || ||||| ||||| | ||||| || ||||| ||
 Db 1503 CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1562

Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA 1674
 ||||| || ||||| ||||| ||||| ||||| || ||||| |||||
 Db 1563 ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA 1622

Qy 1675 ATAGAAGAAAGGAAGGCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1623 ATAGAAGAAAAGAAGGCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC 1682

Qy 1732 CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1683 CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1742

Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851
 ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
 Db 1743 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1802

Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911
 ||||| ||||| ||||| || ||||| ||||| ||||| ||||| |||||
 Db 1803 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1862

Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1863 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1922

Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 Db 1923 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG 1982

Qy 2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA 2091
 ||||| ||||| ||||| || ||||| ||||| || ||||| |||||
 Db 1983 GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA 2042

Qy 2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC 2151
 || ||| | |||| || ||||| ||||| || ||||| | ||||| |||||
 Db 2043 TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC 2099

Qy 2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA 2208
 ||||| ||||| ||||| ||||| ||||| | ||||| |||||
 Db 2100 CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA 2159

Qy 2209 GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA 2268
 | ||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||
 Db 2160 GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA 2219

Qy 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC 2328
 || ||||| ||||| ||||| ||||| ||||| || ||||| |||||
 Db 2220 TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC 2279

Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2280	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2339
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2340	GAAGATTCCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2399
Qy	2449	GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2400	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2459
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCCTTGCCACCTGAGGGA	2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTG	2799
Db	2700	ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2759
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2760	AGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2819
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGCACAGAATTG	2879
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2880	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2939
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210

Db	3120	TTTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC	3270
Db	3180	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC	3239
Qy	3271	ATTGTCAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3240	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3299
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3390
Db	3300	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3359
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3360	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAAGTACAGTAATTCTGCT	3419
Qy	3451	CTTGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3420	CTTGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA	3479
Qy	3511	GTTGATTCCCTGAAGTTTGCACTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3480	GTTGATTCTCTGAAGTTTGCACTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3539
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3540	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT	3599
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3600	GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3659
Qy	3691	GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740
Db	3660	GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA	3709

RESULT 5

ABV94680

ID ABV94680 standard; cDNA; 4632 BP.

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AC ABV94680;

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DT 14-JAN-2003 (first entry)

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DE Human pancreatic cancer expressed cDNA SEQ ID NO 53.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
 KW cytostatic; tumour; gene; ss.

XX

OS Homo sapiens.

XX

PN WO200260317-A2.

XX

Db 83 CTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 141
 Qy 253 ATGGAAGACATAGACCAGTTCGTGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
 ||||| | ||||| | |||| | ||||| ||||| ||||| |||||
 Db 142 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCACCCCGGCCG 198
 Qy 313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 199 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 255
 Qy 373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
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 Db 256 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 315
 Qy 433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCGCCGCTG 486
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 Db 316 CCCGCCCGGGCTGTCCGCGGCCCACTGCCACCGCCCTGCCGCCGGCGCGCCCTG 375
 Qy 487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
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 Db 376 ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 435
 Qy 547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
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 Db 436 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC 495
 Qy 598 GCGCCATCCCTGCCGCCCCGCTGCCGCAGTCTTGCCTCCAAGCTCCCAGAGGACGACGAG 657
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 Db 496 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 555
 Qy 658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG----- 711
 ||||| ||||| || ||||| || || ||||| || ||||| ||||| |||||
 Db 556 CCTCCGGCCCCGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 615
 Qy 712 -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
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 Db 616 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGGCCGCGCCCAAGCGC 675
 Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
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 Db 676 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 735
 Qy 808 GTGATACCCTCCTCTGCAGAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
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 Db 736 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 792
 Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAACTGCTGCCTCTCTTCCTTCT 927
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 Db 793 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAACTGCTGCTTCTCTTCCTTCT 852
 Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCA 987
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 Db 853 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 912
 Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
 || | | || ||||| || ||||| || ||||| || ||||| ||||| ||||| |||||
 Db 913 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 972

Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	973	GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	1032
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1033	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1092
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	1093	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1152
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1153	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1212
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATGTCAGTAGTA	1329
Db	1213	GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAA	1272
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAG	1389
Db	1273	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAG	1332
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1333	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAACTTG	1389
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAG	1497
Db	1390	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1449
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCCAGAACCTGTGAAGGAC	1557
Db	1450	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAGGAT	1509
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614
Db	1510	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1569
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAA	1674
Db	1570	ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAAA	1629
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1630	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC	1689
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1690	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1749
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1750	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1809

Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1810	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1869
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1870	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1929
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAAGTTTGCCTGATATTGTTATG	2031
Db	1930	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAAGTTTGCCTGACATTGTTATG	1989
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1990	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2049
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2050	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2106
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2107	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2166
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTCAAGAAACAGAAGCTCCTTATATA	2268
Db	2167	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2226
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	2227	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTT	2286
Qy	2329	TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2287	TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2346
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2347	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2406
Qy	2449	GTCCACACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2407	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2466
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2467	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2526
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2527	GGAAAGCCATATTTGGAATCTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2586
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2587	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2646
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739

Db	2647	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2706
Qy	2740	AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2707	ACTGAAACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2766
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2767	AGTTCTAAAACGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2826
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2827	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACACAGAATTG	2886
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2887	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2946
Qy	2971	GATGAATTCTCCGAAAAATAGGTCCAGTGATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2947	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	3006
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3007	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTA	3066
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3067	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3126
Qy	3151	TTGTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3127	TTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3186
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTT	3270
Db	3187	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTATTGACAGTATT	3246
Qy	3271	ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3247	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3306
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTAGGGCA	3390
Db	3307	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTAGGGCA	3366
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3367	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3426
Qy	3451	CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3427	CTTGGTCATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA	3486
Qy	3511	GTTGATTCCTGAAGTTTGAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570


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Db      3487 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3546
Qy      3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
        |||
Db      3547 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTTCAGTGTTCCTGTTATTTAT 3606
Qy      3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
        |||
Db      3607 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3666
Qy      3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
        ||
Db      3667 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3716

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RESULT 6

AAA23454

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ID      AAA23454 standard; cDNA; 4093 BP.
XX
AC      AAA23454;
XX
DT      19-JUN-2000 (first entry)
XX
DE      cDNA encoding human secreted protein vb22_1, SEQ ID NO:63.
XX
KW      Human; secreted protein; cancer; tumour; cardiovascular disorder;
KW      blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;
KW      infection; fungal; bacterial; viral; HIV; allergy; arthritis;
KW      neurodegenerative disease; asthma; contraceptive; ss.
XX
OS      Homo sapiens.
XX
FH      Key          Location/Qualifiers
FT      CDS          152..1006
FT                      /*tag= b
FT                      /product= "Clone vb22_1 ORF2"
FT      CDS          1048..3729
FT                      /*tag= a
FT                      /product= "Human secreted protein vb22_1"
XX
PN      WO200011015-A1.
XX
PD      02-MAR-2000.
XX
PF      24-AUG-1999; 99WO-US019351.
XX
PR      24-AUG-1998; 98US-0097638P.
PR      24-AUG-1998; 98US-0097659P.
PR      09-SEP-1998; 98US-0099618P.
PR      28-SEP-1998; 98US-0102092P.
PR      25-NOV-1998; 98US-0109978P.
PR      23-DEC-1998; 98US-0113645P.
PR      23-DEC-1998; 98US-0113646P.
PR      23-AUG-1999; 99US-00379246.
XX
PA      (ALPH-) ALPHAGENE INC.
XX

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PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX

DR WPI; 2000-224657/19.

DR P-PSDB; AAY95012, AAY95030.

XX

PT New secreted or transmembrane proteins and polynucleotides encoding them,
PT useful for treating neurodegenerative disorders, autoimmune diseases and
PT cancer.

XX

PS Claim 72; Page 321-322; 357pp; English.

XX

CC The invention relates to 40 human secreted proteins (AAY94981-Y95020),
CC and cDNA sequences encoding them (AAA23423-A23462). The secreted proteins
CC of the invention include those that are thought to be only partially
CC secreted, i.e., transmembrane proteins. The proteins of the invention may
CC exhibit one or more activities selected from the following: cytokine
CC activity; cell proliferation; differentiation; immune modulation;
CC haematopoiesis regulation; tissue growth activity; activin/inhibin
CC activity; chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC activity; anti-inflammatory activity; and tumour inhibition activity. The
CC proteins may be administered to patients as vaccines, and the nucleotides
CC may be used as part of a gene therapy regime. Diseases or conditions that
CC may be treated using the proteins or nucleotides of the invention include
CC autoimmune diseases; genetic disorders; haemophilia; cardiovascular
CC diseases; cancer; bacterial, fungal and viral infections, especially HIV;
CC multiple sclerosis; rheumatoid arthritis; pulmonary inflammation;
CC Guillain-Barre syndrome; insulin dependent diabetes mellitus; and
CC allergic reactions such as asthma and anaemia. They may also be used for
CC treating wounds, burns, ulcers, osteoporosis, osteoarthritis, periodontal
CC diseases, Alzheimer's disease, Parkinson's disease, Huntington's disease
CC and amyotrophic lateral sclerosis (ALS). Proteins with activin/inhibin
CC activity may additionally be useful as contraceptives. Nucleic acid
CC sequences of the invention may be used in chromosome mapping, and as a
CC source of diagnostic primers and probes. The present sequence represents
CC cDNA encoding one of the 40 proteins of the invention

XX

SQ Sequence 4093 BP; 1213 A; 926 C; 928 G; 1026 T; 0 U; 0 Other;

Query Match 62.4%; Score 2333.2; DB 3; Length 4093;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 573; Indels 120; Gaps 22;

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QY      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      33 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCGCGGGCT 92

QY      194 CTGAGGAGAAGCGGC-CCTGCGGGGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      93 CTGAGACGCGGCCCCGGCGGGCGGGCAGCAGCTGCAGCATCATC-TCCACCCCTCCAGCC 151

QY      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
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Db      152 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCGGCCG 208

QY      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCAGGACGAGGAGGACGAGGAGGAG 372
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Db      209 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCAGGACGAGGAG---GAAGAAGAG 265
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Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	432
Db	266	GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	325
Qy	433	CCCGCAGCCGGGCTGTCCGAGCTGCGGTGC-----CGCCCCGCCGCCGCCGCCGCTG	486
Db	326	CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCCCTGCCGCCGGCGCGCCCTG	385
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	386	ATGGACTTCGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	445
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	446	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC	505
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCAGAGGACGACGAG	657
Db	506	GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTGCCCTCCAAGCTCCCTGAGGACGACGAG	565
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	566	CCTCCGGCCCGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	625
Qy	712	-----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	626	TGACCCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGGCCGCGCCCAAGCGC	685
Qy	751	AGGGGCTCC---GGCTCAGTGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT	807
Db	686	AGGGGCTCCTCGGGCTCAGTGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT	745
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	746	GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	802
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	803	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	862
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGAACCTATCAGCA	987
Db	863	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGAATTTGTCAACA	922
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	923	GTATTACCCACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	982
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	983	GAGAAGGCAA--AACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1041
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1042	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1101

Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
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 Db 1102 AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1161

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269
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 Db 1162 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1221

Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATGTCAGTAGTA 1329
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 Db 1222 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGCAGTGGAA 1281

Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389
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 Db 1282 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1341

Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437
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 Db 1342 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1398

Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG 1497
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 Db 1399 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA 1458

Qy 1498 GATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557
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 Db 1459 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1518

Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA 1614
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 Db 1519 CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA 1578

Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA 1674
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 Db 1579 ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA 1638

Qy 1675 ATAGAAGAAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1639 ATAGAAGAAAAGGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC 1698

Qy 1732 CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791
 |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1699 CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1758

Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851
 ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
 Db 1759 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1818

Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911
 ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 Db 1819 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1878

Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971
 ||||| ||||| ||||| ||||| || ||||| ||||| || || ||||| |||||
 Db 1879 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1938

Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031

Db	1939		TGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1998
Qy	2032		GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1999		GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTCCGTGATACAGCCAGCTCA	2058
Qy	2092		TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2059		TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2115
Qy	2152		CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2116		CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2175
Qy	2209		GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2176		GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2235
Qy	2269		TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2236		TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2295
Qy	2329		TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2296		TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2355
Qy	2389		GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA	2448
Db	2356		GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCATACCTGAC	2415
Qy	2449		GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2416		GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2475
Qy	2503		GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCCTCACCTCAGGAGCTA	2562
Db	2476		TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAAGTCACTGCTTTGCCACCTGAGGGA	2535
Qy	2563		GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2536		GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2595
Qy	2620		TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAATGGAAGAGTTT	2679
Db	2596		CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2655
Qy	2680		AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2656		AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2715
Qy	2740		AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2716		ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2775
Qy	2800		AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856

Db 2776 AGTTCTAAAAC TGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2835
 Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG 2916
 |||||
 Db 2836 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACACAGAATTG 2895
 Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970
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 Db 2896 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2955
 Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030
 |||||
 Db 2956 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 3015
 Qy 3031 TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
 |||||
 Db 3016 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTA 3075
 Qy 3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA 3150
 |||||
 Db 3076 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 3135
 Qy 3151 TTGTGAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210
 ||
 Db 3136 TTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3195
 Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCA 3270
 |||||
 Db 3196 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAG 3255
 Qy 3271 ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
 |||||
 Db 3256 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3315
 Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3390
 |||||
 Db 3316 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3375
 Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAAGAAATACAGTAATTCTGCT 3450
 |||
 Db 3376 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3435
 Qy 3451 CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
 |||||
 Db 3436 CTTGGTCATGTGAACTGCACGATAAAGGAACCTCAGGCGCCTCTTCTTAGTTGATGATTTA 3495
 Qy 3511 GTTGATTCCCTGAAGTTTGAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570
 |||||
 Db 3496 GTTGATTCTCTGAAGTTTGAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3555
 Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
 |||||
 Db 3556 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3615
 Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
 |||||
 Db 3616 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3675

Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
 || ||||| |||||||||||||||||||||||||||||||||| ||
 Db 3676 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3725

RESULT 7

ABS70449

ID ABS70449 standard; cDNA; 4822 BP.

XX

AC ABS70449;

XX

DT 27-NOV-2002 (first entry)

XX

DE Human bone remodelling gene #106.

XX

KW Bone remodelling; osteoporosis; human; gene; ss.

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OS Homo sapiens.

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PN US6426186-B1.

XX

PD 30-JUL-2002.

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PF 18-JAN-2000; 2000US-00484970.

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PR 18-JAN-2000; 2000US-00484970.

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PA (INCY-) INCYTE GENOMICS INC.

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PI Jones KA, Volkmuth W, Walker MG;

XX

DR WPI; 2002-673014/72.

XX

PT A combination of polynucleotides which are co-expressed with genes known
 PT to be involved in bone remodeling and osteoporosis are useful in an array
 PT for the diagnosis of bone remodeling and osteoporosis associated
 PT disorders.

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PS Claim 1; Col 283-288; 206pp; English.

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CC The invention relates to a combination comprising a number of
 CC substantially purified and isolated polynucleotides which are co-
 CC expressed with genes known to be involved in bone remodelling and
 CC osteoporosis. The invention is used to diagnose disorders associated with
 CC bone remodelling or osteoporosis. ABS70344-ABS70512 represent human bone
 CC remodelling genes of the invention

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SQ Sequence 4822 BP; 1441 A; 1046 C; 1073 G; 1247 T; 0 U; 15 Other;

Query Match 62.1%; Score 2323.8; DB 6; Length 4822;
 Best Local Similarity 80.9%; Pred. No. 0;
 Matches 3060; Conservative 0; Mismatches 587; Indels 137; Gaps 25;

Qy 63 CGCGAAGGCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCG 122
 | | || ||||| || |||||||||||||||||||||||||| || | | |||| | |||
 Db 78 CNCGGAGGCAGGAGGAGCAGTCTCATTGTTCCGGGAGCCGTCACCACAGTAGGTCCCTCG 137

Qy	123	GCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAAC	182
Db	138	GCTCAGT-----CGGCCAGCCCCCTCTCAGTCCTCCCCAACCCCCACAAC	182
Qy	183	CGCCCCGCGACTCTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCG	241
Db	183	CGCCCCGCGGCTCTGAGACGCGGCCCCGGNGGCGGCGGCAGCAGCTGCAGCATCATC-TCC	241
Qy	242	ACCCGCCAGCCATGGAAGACATAGACCAGTCGTTCGCTGGTCTCCTCGTCCACGGACAGCC	301
Db	242	ACCTTCAGCCATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCTCGGACAGCC	298
Qy	302	CGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGG	361
Db	299	CACCCCGGCCGCGAGCCCGCTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG-	357
Qy	362	ACGAGGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGC	421
Db	358	--GAAGAAGAGGANGATGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGC	415
Qy	422	TGGAGAGGAAGCCCGCAGCCGGGCTGTCCGCGAGCTGCGGTGC-----CGCCCGCCGCCG	475
Db	416	TGGAGAGGAAGCCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCCG	475
Qy	476	CCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGC	535
Db	476	GCGGCCNNTAATGGACTTCGGAATGACTTCGTGCCGCGGCGCCCCGGGGACCCCTGC	535
Qy	536	CGGCCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----	589
Db	536	CGGCCGCTCCCCCGCTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGT	595
Qy	590	---CGGCGCCCGCGCCATCCCTGCCGCCCCGCTGCCGCGAGTCTGCCCTCCAAGCTCCCAG	646
Db	596	CGACCGTGCCCGCGCCATCCCCGCTGTCTGCTGCCGCGAGTCTGCCCTCCAAGCTCCCTG	655
Qy	647	AGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGG	706
Db	656	AGGACGACGAGCCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGG	715
Qy	707	CGGAGC-----CCGCCGCGCCCCCTTCCACGCCGGCCG	739
Db	716	CAGAGCCCGTGTGGANCCCGCCAGCCCCGGCTNCCGCCGCGCCCCCTCCACCCGGCCG	775
Qy	740	CGCCCAAGCGCAGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGTCTCTCCTGCTG	796
Db	776	CGCCCAAGCGCAGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGTCTCTCCTGCTG	835
Qy	797	CATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAATTATGGATTTGATGGAGCAGCCAG	856
Db	836	CATCTGAGCCTGTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAG	892
Qy	857	GTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCT	916
Db	893	GTAACACTATTTTCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCT	952

Qy 917 CTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTA 976
 |||||
 Db 953 CTCTTCCTTCTCTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTA 1012

Qy 977 ACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTA 1036
 |||||
 Db 1013 ATTTGTCAACAGTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTA 1072

Qy 1037 AAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAAATTTTCAG 1096
 |||||
 Db 1073 AAGAGGTCTCAGAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAG 1132

Qy 1097 AATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCA 1156
 |||||
 Db 1133 AATTAGAATACTCAGAAATGGGATCATCGTTAGTGTCTCTCCAAAAGCAGAAATCTGCCG 1192

Qy 1157 TATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATT 1213
 |||||
 Db 1193 TAATAGTAGCAAATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGT 1252

Qy 1214 TAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGG 1258
 |||||
 Db 1253 TAGTTAGTAATAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGG 1312

Qy 1259 GTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGA 1318
 |||||
 Db 1313 TTAAAGAGGATGAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAGAGAG 1372

Qy 1319 TGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCAT 1378
 |||||
 Db 1373 TTGCAGTGGAAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTAT 1432

Qy 1379 GGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT----- 1431
 |||||
 Db 1433 GGAAGTGAAAGATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCG 1489

Qy 1432 -----AATGTGGAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAA 1486
 |||||
 Db 1490 AGAGCAACTTGGAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTA 1549

Qy 1487 GTCTTGGAAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAAGAAC 1546
 |||||
 Db 1550 ATCACGAAAAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAG 1609

Qy 1547 CTGTGAAGGACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCG 1603
 |||||
 Db 1610 GTATAAAGGATCGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTG 1669

Qy 1604 AAAGCACCACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAACAG 1663
 |||||
 Db 1670 AGAGCATTGCAACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCG 1729

Qy 1664 ATG-AAAAAAAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCC 1719
 |||||
 Db 1730 ATGAAAAAAAAAATAGAAGAAAGGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACC 1789

Qy 1720 AAAACGTCAAATCC-TTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAAC 1778

Db	1790	AAAAACATCAAACCCTTTTACTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAAC	1849
Qy	1779	AGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCC	1838
Db	1850	AGATAATTTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCC	1909
Qy	1839	AGATTTTAGTTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGC	1898
Db	1910	AGATTTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGC	1969
Qy	1899	TTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCC	1958
Db	1970	TTATGAAACAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCC	2029
Qy	1959	CACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGGCC	2018
Db	2030	TGCAGCACAGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTGGCC	2089
Qy	2019	TGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGT	2078
Db	2090	TGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGAT	2149
Qy	2079	GCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCT	2138
Db	2150	ACAGCCCAGCTCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACA	2206
Qy	2139	TGAGCCTGAAAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTT	2195
Db	2207	TGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATC	2266
Qy	2196	GGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGA	2255
Db	2267	AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGA	2326
Qy	2256	AGTCCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCC	2315
Db	2327	AGTCCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACC	2386
Qy	2316	AAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACA	2375
Db	2387	AGTCCGGATTTCTCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCA	2446
Qy	2376	CGCTGAGCTAGTGGAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGA	2435
Db	2447	TTCTGAGCTAGTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGA	2506
Qy	2436	TTTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCT	2495
Db	2507	TTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCT	2566
Qy	2496	CACTGA-----AGTGTCTGAGACAGTAGCCCGAGCACAAAGAGGAGAGACTTAGTGCCTC	2549
Db	2567	CACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTT	2626
Qy	2550	ACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAA	2609

Db 2627 GCCACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAA 2686
 Qy 2610 AGATGC---TGCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCA 2666
 |||| | | || |||| | | |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 2687 AGATACCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCA 2746
 Qy 2667 AATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGA 2726
 |||| | | | | |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 2747 GATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGC 2806
 Qy 2727 CAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATT 2786
 | |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 2807 ACAGATAAGAGAAACTGAAACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTT 2866
 Qy 2787 TCCCACGTTTGTCTAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGA 2843
 || || || || |||| |||| |||| |||| | |||| |||| |||| |||| ||||
 Db 2867 CCCTACATTGATCAGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGA 2926
 Qy 2844 TCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCC 2903
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 2927 CCTAGAAGTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCTATTGCC 2986
 Qy 2904 TTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG---- 2959
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 2987 TTGCACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAA 3046
 Qy 2960 --TACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATC 3017
 | | | |||| || || || |||| |||| || || || |||| || || || || || ||
 Db 3047 AATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATT 3106
 Qy 3018 GCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAA 3077
 |||| || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 3107 GCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAA 3166
 Qy 3078 ATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATC 3137
 | || | |||| |||| |||| |||| |||| |||| || |||| |||| |||| |||| ||||
 Db 3167 AGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATC 3226
 Qy 3138 CCTGTCTGCTGTATTGTCTGAGAGCTGAG-TAAAACCTTCAGTTGTTGACCTCCTCTACT 3196
 | || || || |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 3227 ACCATCTGCTATATTTTTCAGCAGAGCTGAGCTAAAACCTTCAGTTGTTGACCTCCTGTACT 3286
 Qy 3197 GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTC 3256
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 3287 GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTTCCTGCTGCTTTTCAT 3346
 Qy 3257 TGACAGTGTTTCAGCATTGTCTGAGTGAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGA 3316
 |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 3347 TGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGA 3406
 Qy 3317 CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC 3376
 | |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 3407 CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC 3466
 Qy 3377 ACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAAT 3436
 |||| |||| |||| || |||| |||| |||| |||| |||| |||| |||| |||| ||||
 Db 3467 ACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGT 3526

Qy 3437 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCT 3496
 |||
 Db 3527 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGGAACTCAGGCGCCTCTTCT 3586
 Qy 3497 TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATG 3556
 |||
 Db 3587 TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTACCTATG 3646
 Qy 3557 TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA 3616
 |||
 Db 3647 TTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCCTCTTCAGTG 3706
 Qy 3617 TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676
 |||
 Db 3707 TTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 3766
 Qy 3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736
 |||
 Db 3767 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3826
 Qy 3737 CAGA 3740
 |||
 Db 3827 CTGA 3830

RESULT 8

ABX34563

ID ABX34563 standard; cDNA; 4698 BP.

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AC ABX34563;

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DT 13-FEB-2003 (first entry)

XX

DE Human mddt cDNA SEQ ID 124.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
 KW psoriasis; hepatitis; gene; ss.

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OS Homo sapiens.

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PN WO200279449-A2.

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PD 10-OCT-2002.

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PF 27-MAR-2002; 2002WO-US009944.

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PR 28-MAR-2001; 2001US-0279619P.

PR 29-MAR-2001; 2001US-0280067P.

PR 29-MAR-2001; 2001US-0280068P.

PR 16-MAY-2001; 2001US-0291280P.

PR 17-MAY-2001; 2001US-0291829P.
PR 17-MAY-2001; 2001US-0291849P.
PR 19-JUN-2001; 2001US-0299428P.
PR 20-JUN-2001; 2001US-0299776P.
PR 20-JUN-2001; 2001US-0300001P.

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PA (INCY-) INCYTE GENOMICS INC.

XX

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;
PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;

XX

DR WPI; 2003-058431/05.

DR P-PSDB; ABU11573.

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PT New purified disease detection and treatment molecule proteins and
PT polynucleotides, useful for diagnosing, treating or preventing cancers
PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
PT or hepatitis.

XX

PS Claim 1; SEQ ID NO 124; 339pp + Sequence Listing; English.

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CC This invention describes a novel disease detection and treatment molecule
CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
CC and the polypeptides of the invention can be used for gene therapy,
CC protein replacement therapy and are useful for treating a variety of
CC diseases or conditions. These polypeptides or polynucleotides are
CC particularly useful for diagnosing, treating or preventing cell
CC proliferative disorders (e.g. cancers including adenocarcinoma,
CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
CC hepatitis. ABX34440-ABX34835 encode the MDDT polypeptides represented in
CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

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SQ Sequence 4698 BP; 1410 A; 1028 C; 1022 G; 1238 T; 0 U; 0 Other;

Query Match 61.4%; Score 2297.4; DB 7; Length 4698;
Best Local Similarity 80.7%; Pred. No. 0;
Matches 2996; Conservative 0; Mismatches 596; Indels 121; Gaps 22;

Qy 134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCCAACCCCCACAACCGCCCGCGACT 193
| || ||| | | ||| ||||| ||||| | ||||| ||||| |||||
Db 23 CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGCTC 82

Qy 194 CTGAGGAGAAGCGGCCCTGCGGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA 253
||||| | | | ||||| | ||||| || | ||| |||||
Db 83 CTGAGACGCGCCCCGGCGGGCGGGCAGCAGCTGCAGCATCATC-TCCACCCTCCAGCCA 141

Qy 254 TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGCCTC 313

Accession	Position	Sequence	Length
Db	142	TGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCCACCCCGGCCGC	198
Qy	314	CGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG	373
Db	199	AGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAGG	255
Qy	374	AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC	433
Db	256	AGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAGC	315
Qy	434	CCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCCGCCGCTGC	487
Db	316	CCGCCGCCGGGCTGTCCGCAGGCCCCAGTGCCACCGCCCTGCCGCCGGCGCGCCCTGA	375
Qy	488	TGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCC	547
Db	376	TGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGCGGACCCCTGCCGGCCGCTTCCC	435
Qy	548	CTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCCG	598
Db	436	CCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTCGACCGTGCCCG	495
Qy	599	CGCCATCCCTGCCGCCCCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAGC	658
Db	496	CGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAGC	555
Qy	659	CTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	556	CTCCGGCCCGGCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTGT	615
Qy	712	-----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGCA	751
Db	616	GGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCCGCGCCCAAGCGCA	675
Qy	752	GGGGCTCC---GGCTCAGTGGATGAGACCC--TTTTTGCTCTTCTGCTGCATCTGAGC	805
Db	676	GGGGCTCCTCGGGCTCAGATGGATGAGACCCATTTTTGCTCTTACCTGCTGCATCTGAGC	735
Qy	806	CTGTGATACCCTCCTCTGCAGAAAAATATGGATTTGATGGAGCAGCCAGGTAACACTG	865
Db	736	CTGTGATACGCTCCTC--ATGCAGAAATATGGACTTGAAGGAGCAGCCAGGTAACACTA	793
Qy	866	TTTCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCTT	925
Db	794	TTTCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCTTCTCTTCTT	853
Qy	926	CTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAG	985
Db	854	CTCTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAA	913
Qy	986	CAGTGTTCATCCTCAGAAGGAACAATTGAAG-AACTTTAAATGAAGCTTCTAAAGAGTTG	1044
Db	914	CAGTATTACCCACTGAAGGAACACTTCAAGAAAAATGTCAGTGAAGCTTCTAAAGAGGTC	973
Qy	1045	CCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAA	1104

Db 974 TCAGAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAA 1033
 Qy 1105 TATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTA 1164
 || ||||| ||||| || | | ||| ||||| ||| || ||| || |||||
 Db 1034 TACTCAGAAATGGGATCATCGTTCAAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTA 1093
 Qy 1165 GAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGT 1221
 | ||| ||| ||||| ||||| |||| | |||| | | ||||| ||
 Db 1094 GCAAATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGT 1153
 Qy 1222 AGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA 1266
 | | ||||| | || ||||| | |||| ||| |||||
 Db 1154 AATAACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAG 1213
 Qy 1267 GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTA 1326
 || ||||| ||||| ||||| ||| ||||| ||||| || | |||||
 Db 1214 GATGAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTG 1273
 Qy 1327 GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG 1386
 | ||| ||| ||||| || ||||| ||||| ||||| ||| ||||| |||||
 Db 1274 GAAGCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG 1333
 Qy 1387 AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AAT 1434
 ||||| | ||| | ||| ||| || ||||| |||| | ||
 Db 1334 AAAGATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAATCGAGAGCAAC 1390
 Qy 1435 GTGGAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAAGTCTTGGG 1494
 ||||| ||||| || ||||| || ||||| ||||| ||||| || |||
 Db 1391 TTGGAAAGTAAAGTGGAATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTAATCACGAA 1450
 Qy 1495 AAGGATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAAGACCTGTGAAG 1554
 || ||||| || ||||| || ||||| ||||| ||||| ||||| || |||
 Db 1451 AAAGATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAG 1510
 Qy 1555 GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACC 1611
 || | || ||||| || ||||| ||||| ||||| ||||| || |||||
 Db 1511 GATCGTTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATT 1570
 Qy 1612 ACAGCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAA 1671
 || ||||| || ||||| ||||| ||||| ||||| ||||| || |||||
 Db 1571 GCAACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAA 1630
 Qy 1672 AAAATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCA 1728
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1631 AAAATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCA 1690
 Qy 1729 AATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTA 1788
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
 Db 1691 AACCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTA 1750
 Qy 1789 TCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTT 1848
 ||||| ||||| || ||||| ||||| ||||| ||||| |||||
 Db 1751 ACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTA 1810
 Qy 1849 CAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACA 1908
 ||||| ||||| ||||| ||||| || ||||| ||||| |||||
 Db 1811 CAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACA 1870

Qy	1909	AAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAG	1968
Db	1871	AAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAG	1930
Qy	1969	CTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTGCCTGATATTGTT	2028
Db	1931	CTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTGCCTGACATTGTT	1990
Qy	2029	ATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGT	2088
Db	1991	ATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGC	2050
Qy	2089	GTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAA	2148
Db	2051	TCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAA	2107
Qy	2149	AACCCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAG	2205
Db	2108	AACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAG	2167
Qy	2206	GAAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAAGAAACAGAAGCTCCTTAT	2265
Db	2168	GAAGAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTAT	2227
Qy	2266	ATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGAT	2325
Db	2228	ATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGAT	2287
Qy	2326	TTCTCTAATTATTAGAAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTA	2385
Db	2288	TTCTCTGATTATTAGAAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTA	2347
Qy	2386	GTGGAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCT	2445
Db	2348	GTTGAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCT	2407
Qy	2446	GAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA----	2501
Db	2408	GACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACT	2467
Qy	2502	--AGTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAG	2559
Db	2468	TCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAG	2527
Qy	2560	CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T	2616
Db	2528	GGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTTG	2587
Qy	2617	GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAAATGGAAGAG	2676
Db	2588	TTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAG	2647
Qy	2677	TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA	2736
Db	2648	CTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGA	2707

Qy	2737	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTT	2796
Db	2708		
Qy	2797	GAAACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTG	2767
Qy	2797	GTCAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2853
Db	2768		
Qy	2854	ATCAGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTA	2827
Qy	2854	TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAA	2913
Db	2828		
Qy	2854	TCCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGACAGAA	2887
Qy	2914	TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTT	2967
Db	2888		
Qy	2914	TTGCCCCATGACCTTTCTTTGAAGAACATAACAACCCAAAGTTGAAGAGAAAATCAGTTTC	2947
Qy	2968	TCAGATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAAT	3027
Db	2948		
Qy	2968	TCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGAT	3007
Qy	3028	GTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACG	3087
Db	3008		
Qy	3028	GTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTG	3067
Qy	3088	AAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCT	3147
Db	3068		
Qy	3088	AAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCT	3127
Qy	3148	GTATTGTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATT	3207
Db	3128		
Qy	3148	ATATTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATT	3187
Qy	3208	AAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCTGCTGCTGTCTCTGACAGTGTTC	3267
Db	3188		
Qy	3208	AAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTATTC	3247
Qy	3268	AGCATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTT	3327
Db	3248		
Qy	3268	AGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTT	3307
Qy	3328	AGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGG	3387
Db	3308		
Qy	3328	AGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGG	3367
Qy	3388	GCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCT	3447
Db	3368		
Qy	3388	GCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAATACAGTAATTCT	3427
Qy	3448	GCTCTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGAT	3507
Db	3428		
Qy	3448	GCTCTTGGTCATGTGAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAATACAGTAATTCT	3487
Qy	3508	TTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTG	3567
Db	3488		
Qy	3508	TTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTG	3547
Qy	3568	TTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATT	3627

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Db      3548 TTTAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCCTGTTATT 3607
      |||||
Qy      3628 TATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAG 3687
      |||||
Db      3608 TATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAA 3667
      |||||
Qy      3688 GATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
      |||||
Db      3668 GATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3720

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RESULT 9

AAZ56886

ID AAZ56886 standard; DNA; 3579 BP.

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AC AAZ56886;

XX

DT 25-APR-2000 (first entry)

XX

DE Human MAGI polypeptide encoding DNA.

XX

KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;
 KW psychiatric disorder; developmental disorder; inflammatory disorder;
 KW stroke; cytostatic; cerebroprotective; neuroprotective; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1. .3579

FT /*tag= a

FT /product= "MAGI polypeptide"

XX

PN WO200005364-A1.

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PD 03-FEB-2000.

XX

PF 21-JUL-1999; 99WO-GB002360.

XX

PR 22-JUL-1998; 98GB-00016024.

PR 19-JUL-1999; 99GB-00016898.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

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PI Michalovich D, Prinjha RK;

XX

DR WPI; 2000-182693/16.

DR P-PSDB; AAY56967.

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PT Novel polypeptides related to neuroendocrine-specific proteins and
 PT polynucleotides useful for diagnosis of various diseases and for
 PT treatment of cancer and neurological disorders.

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PS Claim 5; Page 19-20; 35pp; English.

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CC The invention relates to human MAGI protein, which is similar to

neuroendocrine-specific protein. The MAGI protein can be expressed by standard recombinant methodology. The MAGI polypeptides, polynucleotides and antibodies are useful for treating diseases, including neuropathies, spinal injury, neuronal degeneration, neuromuscular disorders, psychiatric disorders and developmental disorders, cancer, stroke and inflammatory disorders. The polynucleotide is also useful for chromosome localization and for tissue expression studies. The present sequence represents a DNA encoding the human MAGI protein

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 61.2%; Score 2289.2; DB 3; Length 3579;
Best Local Similarity 81.5%; Pred. No. 0;
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

[illegible]

Db	595	GTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAGCTGCTGCCTCTCTTCCTTCT	927
Db	652	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAGCTGCTGCTTCTCTTCCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGAACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAG	1497
Db	1249	GAAAGTAAAGTGGAATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1429	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1488

Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1548
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA	2448
Db	2206	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325

Qy 2503 GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA 2562
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2326 TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA 2385

Qy 2563 GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA 2619
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2386 GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA 2445

Qy 2620 TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT 2679
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2446 CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC 2505

Qy 2680 AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA 2739
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2506 AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA 2565

Qy 2740 AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC 2799
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2566 ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC 2625

Qy 2800 AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC 2856
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2626 AGTTCATAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2685

Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATGCCTTGCTTAGAATTG 2916
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2686 CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCAATGCCTTGACAGAAATTG 2745

Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2746 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2805

Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2806 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 2865

Qy 3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2866 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 2925

Qy 3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA 3150
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2926 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 2985

Qy 3151 TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210
 | | | | | | | | | | | | | | | | | | | | | |
 Db 2986 TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3045

Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTACGC 3270
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3046 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTATTGACAGTATTACGC 3105

Qy 3271 ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
 | | | | | | | | | | | | | | | | | | | | | |
 Db 3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165

Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCA 3390

Db	3166	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3225
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3226	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3285
Qy	3451	CTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3286	CTTGGTCATGTGAAGTGCACGATAAAGGAAGCTCAGGCGCCTCTTCTTAGTTGATGATTTA	3345
Qy	3511	GTTGATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3346	GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3405
Qy	3571	AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3406	AATGGTCTGACACTACTGATTTTGGCTCTCATTTCAGTGTTCCTGTTATTTAT	3465
Qy	3631	GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3466	GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3525
Qy	3691	GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740
Db	3526	GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA	3575

RESULT 10

AAF90324

ID AAF90324 standard; cDNA; 3579 BP.

XX

AC AAF90324;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-A cDNA.

XX

KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;
 KW cerebroprotective; neuroleptic; diagnosis; therapy; ss.

XX

OS Homo sapiens.

XX

PN WO200136631-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-GB004345.

XX

PR 15-NOV-1999; 99GB-00026995.

PR 24-JAN-2000; 2000GB-00001550.

XX

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha R;

XX

DR WPI; 2001-343822/36.

DR P-PSDB; AAB82349.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO
PT gene and may be useful in the treatment of neural disorders including
PT Alzheimer's and Parkinson's diseases.

XX

PS Disclosure; Page 25-26; 25pp; English.

XX

CC The present sequence is that of cDNA encoding human NOGO-A (see
CC AAB82349). NOGO-A is a previously known splice variant of the human NOGO
CC gene on chromosome 2p21. NOGO-A cDNA was obtained by PCR amplification of
CC human spinal cord cDNA. The invention relates to a novel splice variant,
CC NOGO-C (see AAF90323). It provides NOGO-C polypeptides and
CC polynucleotides, and methods for producing such polypeptides by
CC recombinant techniques. Also disclosed are methods for utilising NOGO-C
CC polypeptides and polynucleotides in the treatment of diseases including
CC neuropathies, spinal injury, brain injury, stroke, neuronal degeneration,
CC for example Alzheimer's disease and Parkinson's disease, neuromuscular
CC disorders, psychiatric disorders and developmental disorders. Also
CC provided are methods for identifying agonists and agonists for use in
CC treating conditions associated with NOGO-C imbalance, and diagnostic
CC assays for detecting diseases associated with inappropriate NOGO-C
CC activity or levels

XX

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 61.2%; Score 2289.2; DB 4; Length 3579;

Best Local Similarity 81.5%; Pred. No. 0;

Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

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Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCGGCCG 57

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCTGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
          | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      58  CAGCCCGCGTTCAAGTACCAGTTCTGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy      433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCGCCGCGCCGCTG 486
          |||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      175 CCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCCGGCGCGCCCTG 234

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCC 546
          ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      235 ATGGACTTCGGAATGACTTCGTGCCGCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
          || | || | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 354
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Qy	598	CGCCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	355		
		GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	414
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	415		
		CCTCCGGCCCGGCCTCCCCCTCTCCCCCGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	474
Qy	712	-----CCCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	475		
		TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGGCCGCGCCCAAGCGC	534
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	807
Db	535		
		AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT	594
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	595		
		GTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	652		
		TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	712		
		CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772		
		GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832		
		GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892		
		TCAGAAATGGGATCATCGTTCAGTGTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952		
		AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1012		
		AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAAATGGACATTTTTAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072		
		GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132		
		GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437

Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAG	1497
Db	1249	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAAATAAACAGATGAAAAAAAA	1674
Db	1429	ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAAAAA	1488
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC	1548
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTACCCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268

Db 2026 GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA 2085

Qy 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC 2328
 || ||||| ||||| ||||| ||||| || ||||| ||| |||||

Db 2086 TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC 2145

Qy 2329 TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG 2388
 ||| ||||| ||||| ||||| || || || ||||| || || |||||

Db 2146 TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT 2205

Qy 2389 GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTTCCTGAA 2448
 || ||||| ||||| ||||| ||||| ||||| ||||| || |||||

Db 2206 GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC 2265

Qy 2449 GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A 2502
 || ||||| ||||| || ||||| ||||| ||||| ||||| |||||

Db 2266 GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA 2325

Qy 2503 GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA 2562
 | | ||| | ||| ||||| ||||| ||||| ||||| |||||

Db 2326 TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA 2385

Qy 2563 GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA 2619
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2386 GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA 2445

Qy 2620 TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT 2679
 || ||||| || ||||| ||||| ||||| ||||| ||||| |||||

Db 2446 CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC 2505

Qy 2680 AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA 2739
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2506 AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA 2565

Qy 2740 AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC 2799
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2566 ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC 2625

Qy 2800 AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC 2856
 ||| ||||| ||||| | ||||| ||||| ||||| ||||| |||||

Db 2626 AGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2685

Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATGCCTTGCTTAGAATTG 2916
 ||||| ||||| ||||| || ||||| ||||| ||||| |||||

Db 2686 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCAATGCCTTGACAGAATTG 2745

Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970
 ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2746 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2805

Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030
 ||||| || || ||||| ||||| | ||||| ||||| ||||| |||||

Db 2806 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 2865

Qy 3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 2866 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 2925

KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;
 KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;
 KW Nogo-associated disease; metastasis; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1. .3579
 FT /*tag= a
 FT /product= "Human NogoA protein"
 XX
 PN WO200257483-A2.
 XX
 PD 25-JUL-2002.
 XX
 PF 18-JAN-2002; 2002WO-GB000228.
 XX
 PR 18-JAN-2001; 2001GB-00001312.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;
 XX
 DR WPI; 2002-599722/64.
 DR P-PSDB; ABG30938.
 XX
 PT Identifying modulators of Nogo or BACE activity for treating acute
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises
 PT providing and monitoring interaction between Nogo and BACE polypeptides.
 XX
 PS Disclosure; Page 53-58; 68pp; English.
 XX
 CC The present invention relates to a new method of identifying modulators
 CC of Nogo function or BACE activity. The method involves providing Nogo and
 CC BACE polypeptides capable of binding with each other, monitoring the
 CC interaction between these polypeptides, and determining if the test agent
 CC is a modulator of Nogo or BACE activity. The method is useful in treating
 CC acute neuronal injuries, such as spinal or head injury, stroke,
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue
 CC hypertrophy) of the central nervous system. The BACE polypeptide is
 CC useful in screening methods to identify agents that may act as modulators
 CC of BACE activity and in particular agents that may be useful in treating
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,
 CC and the polynucleotide encoding the BACE polypeptide are useful in
 CC manufacturing a medicament for the treatment or prevention of disorders
 CC responsive to the modulation of Nogo activity, in alleviating the
 CC symptoms or improving the condition of a patient suffering from this
 CC disorder, in axon regeneration, or in preventing metastasis or spreading
 CC of a cancer. The polynucleotide may also be an essential component in
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy
 CC techniques. The present nucleic acid sequence encodes the human NogoA
 CC protein of the invention

SQ Sequence 3579 BP; 1074 A; 803 C; 812 G; 890 T; 0 U; 0 Other;

Query Match 61.2%; Score 2289.2; DB 6; Length 3579;
Best Local Similarity 81.5%; Pred. No. 0;
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

[illegible]

Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTAAATGAAAAGAGAGTTGCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG	1497
Db	1249	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1429	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1488
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC	1548
Qy	1732	CCTTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608

Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAAGAGCCTGAAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2206	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2445

Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446		
	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAGAA	2739
Db	2506		
	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTG	2799
Db	2566		
	2566	ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626		
	2626	AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916
Db	2686		
	2686	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGCACAGAATTG	2745
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746		
	2746	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806		
	2806	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866		
	2866	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA	3150
Db	2926		
	2926	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	2986		
	2986	TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3045
Qy	3211	AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCTGCTGCTGTCTCTGACAGTGTTCAGC	3270
Db	3046		
	3046	AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCTGCTGCTTTTCATTGACAGTATTCAGC	3105
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3106		
	3106	ATTGTGAGCGTAACAGCCTACATTGCCTTGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3165
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3390
Db	3166		
	3166	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA	3225
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3226		
	3226	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3285
Qy	3451	CTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510

Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACCTGGAGGTGCTGGAGAGGAAG	432
Db	115	GAGGAGGAAGAGGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	174
Qy	433	CCCGCAGCCGGGCTGTCCGCGAGCTGCGGTGC-----CGCCCGCCGCCGCCGCGCCGCTG	486
Db	175	CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCCGGCGCGCCCTG	234
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	235	ATGGACTTCGGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC	294
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	295	CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC	354
Qy	598	GCGCCATCCCTGCCGCCCGCTGCCGCGAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	355	GCGCCATCCCCGCTGTCTGCTGCCGCGAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	414
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG-----	711
Db	415	CCTCCGGCCCCGGCCTCCCCCTCTCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTG	474
Qy	712	-----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	475	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCCGCGCCCAAGCGC	534
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT	807
Db	535	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCTGCTGCATCTGAGCCT	594
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	595	GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCTTCT	927
Db	652	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951

Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
 || ||| ||||| |||| |||| | |||| || |||| | |||| ||| |
 Db 952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269
 ||||| | || ||||| | |||| ||||| ||
 Db 1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329
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 Db 1072 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA 1131

Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389
 || ||| ||||| || ||||| ||||| || ||||| || ||||| |||||
 Db 1132 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1191

Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437
 |||| | ||| | ||| ||| || ||||| ||| | || ||
 Db 1192 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1248

Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497
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 Db 1249 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACATCACGAAAAA 1308

Qy 1498 GATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557
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 Db 1309 GATAGTGAAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAGGTATAAAGGAT 1368

Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA 1614
 | | ||||| || ||||| ||||| | ||||| || |||| ||
 Db 1369 CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA 1428

Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA 1674
 ||||| ||| ||||| ||||| ||||| ||||| || ||||| |||||
 Db 1429 ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA 1488

Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1489 ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC 1548

Qy 1732 CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791
 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1549 CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1608

Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851
 ||||| ||||| || ||| ||||| ||||| ||||| ||||| |||||
 Db 1609 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1668

Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911
 ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 Db 1669 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1728

Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1729 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1788

Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031

Db	1789	TGCCCATCATTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTGAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTGAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2206	GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2445
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856

Db 2626 AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2685
 Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTGCTTGCCTTGCTTAGAATTG 2916
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 Db 2686 CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTGCTTGCCTTGACAGAATTG 2745
 Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970
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 Db 2746 CCCCATGACCTTTCTTTGAAGAACATAACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2805
 Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030
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 Db 2806 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 2865
 Qy 3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
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 Db 2866 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 2925
 Qy 3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA 3150
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 Db 2926 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 2985
 Qy 3151 TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210
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 Db 2986 TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3045
 Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC 3270
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3046 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTTTCATTGACAGTATTCAGC 3105
 Qy 3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165
 Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA 3390
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA 3225
 Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
 ||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3285
 Qy 3451 CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3286 CTTGGTCATGTGAAGTGCACGATAAAGGAAGTCAAGGCGCCTCTTCTTAGTTGATGATTTA 3345
 Qy 3511 GTTGATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570
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 Db 3346 GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405
 Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT 3465
 Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
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 Db 3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525

Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
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 Db 3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575

RESULT 13

AAD01174

ID AAD01174 standard; cDNA; 3833 BP.

XX

AC AAD01174;

XX

DT 02-NOV-2000 (first entry)

XX

DE Bovine neurite growth inhibitor Nogo cDNA.

XX

KW Bovine; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;
 KW central nervous system; neoplastic disease; antiproliferative; glioma;
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;
 KW structural plasticity; screening; ss.

XX

OS Bos sp.

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PN WO200031235-A2.

XX

PD 02-JUN-2000.

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PF 05-NOV-1999; 99WO-US026160.

XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders
 PT of the central nervous system and inducing regeneration of neurons.

XX

PS Claim 26; Fig 12; 122pp; English.

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CC The present sequence is a cDNA encoding bovine Nogo protein which is a
 CC potent neural cell growth inhibitor and is free of all central nervous
 CC system (CNS) myelin material with which it is natively associated. The
 CC present sequence was obtained from bovine spinal cord white matter cDNA
 CC library. Nogo proteins and fragments displaying neurite growth inhibitory
 CC activity are used in the treatment of neoplastic disease of the CNS e.g.
 CC glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma,
 CC pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma,
 CC menagioma, neuroblastoma or retinoblastoma and degenerative nerve
 CC diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which
 CC promote Nogo activity can be used to treat or prevent hyperproliferative

or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However the specification does not include sequences for these SEQ ID numbers

SQ Sequence 3833 BP; 1235 A; 717 C; 818 G; 1063 T; 0 U; 0 Other;

Query Match 50.0%; Score 1869.8; DB 3; Length 3833;
Best Local Similarity 80.9%; Pred. No. 0;
Matches 2320; Conservative 0; Mismatches 492; Indels 55; Gaps 10;

Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	1	CTATCTCCTCTCTCAGCCGCTGCTTTTAAAGAACGTGAATACCTTGGTGATTTACCAGCA	60
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	61	GTACTGCCCACTGAAGGAACACTTCCAGCAACTTCAAATGAAGCTTCTAAAGCATTCTCA	120
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	121	GAGAAGGCAAAAAATCCATTTGTAGAGAGAAATTTAACAGAATTTTCAGAATTGGAATAT	180
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	181	TCAGAAATGGAATCATCATTCACTGGCTCTCAAAGGCAGAACCTGCCGTAACAGTAGCG	240
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACA---AAGAGGATTTAGTTTGTAGT	1224
Db	241	AATCCTAGGGACGAAATAGTTGTGAGGAGTAGAGATAAAGAAGAGGACTTAGTTAGTCTT	300
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAA	1266
Db	301	AACATCCTTCATACTCAGCAGGAGTTATCTACAGTCCTTACGAAATCAGTTGAAGAAGAA	360
Qy	1267	GACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTA	1326
Db	361	GATAGAGTTCTGTCTCCAGAAAAACAAAGGACAGTTTTAAGGAAAAGGGAGTTGCAGCA	420
Qy	1327	GTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTG	1386
Db	421	GAAGCTTCTATGGGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTG	480
Qy	1387	AAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAAT-----	1434
Db	481	AAAGATACTTACAAGCAAGATAGTGATGTTTTGATTGCTGGAGGTAATATAGAGAGCAA	540
Qy	1435	GTGGAAAGTAAAGTGGACAGAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAAGTCTTGGG	1494
Db	541	TTGGAAGGTAAAGTGGATAAGAAACACTTTTCAGATAGCCTTGAACAAACAAATCGTGAA	600

Qy		1495 AAGGATAGTGAAGGCAGAAATGAGGATGCTTCCTTTCCCGTAGCCCCAGAACCTGTGAAG	1554
Db	601 AAAGATAGTGAAAGCAGTAATGATGACACTTCATTGCCAGTACCAGAACCTGTAAGA	660	
Qy		1555 GACAGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCA	1614
Db	661 GGTGGTTCGGGAGCGTACATCACGTGTGCTCCCTTTAACCCAACAACCTGAGAATGTTTCA	720	
Qy		1615 GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAAAAGATGAAAAAAAA	1674
Db	721 ACAAAACATTTTTCCCTTGTTGGAAGATCATACTTCGAAAATAAGACAGATGAAAAAAG	780	
Qy		1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAGA---CTAGCCCCAAAACGTCAAAT	1731
Db	781 ATAGAA-AAAAAAGGCACAAATTGTAACAGAGAAGAATGCAAGTGTCAAGACATCAAAC	839	
Qy		1732 CCTTTCCTTG TAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	840 CCTTTCCTTATGGCAGCACAGGAGTCTAAGACAGATTACGTTACAACAGATCATGTGTCA	899	
Qy		1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	900 AAGGTGACCGAGGAAGTAGTGGCAAACATGCCTGAAGGTCTAACCCCAGATTTGGTTCAG	959	
Qy		1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	960 GAAGCATGTGAAAGTGAATTGAATGAAGCTACTGGTACAAAATTGCCTTTGAAACAAAA	1019	
Qy		1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1020 ATGGACCTGGTTCAAACCTCAGAAGCTGTGCAGGAGTCACTTTACCTGTAACACAGCTT	1079	
Qy		1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1080 TGCCCATCTTTTGAAGAATCTGAAGCTACTCCGTCACCGGTTTTGCCTGACATTGTCATG	1139	
Qy		2032 GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1140 GAAGCACCATTAAATTCTGTAGTTCCTAGTGCTGGTGCTTCTGCAGTGCAGCTCAGTTCA	1199	
Qy		2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAC	2151
Db	1200 TCACCATTAGAACTCTTCCTTCAGTTAATTATGAAAGCATAAAGTTTGAGCCTGAAAT	1259	
Qy		2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1260 CCCCCACCATATGAGGAGGCCATGAATGTATCACTAAAAAAGAATCAGGAATGAATGAA	1319	
Qy		2209 GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	1320 GAAATCACAGAGCCTGAAGGTATTAGTGTAGCTGTTCAGGAAACAGAAGCTCCTTATATA	1379	
Qy		2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	1380 TCTATTGCATGTGATTTAATTAAAGAAACAAAGATCTCTACTGAACCGACTCCAGATTTT	1439	

Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	1440		
Qy	2389	TCTAGTTATTTCAGAAATAGCAGAAGTTGCACAGCCAGTGCCCGAGCATTCTGAGCTAGTT	1499
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA	2448
Db	1500		
Qy	2389	GAAGATTCCCTCCCCGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCCGAA	1559
Qy	2449	GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTC-	2507
Db	1560		
Qy	2449	GTTCCACAAAAACAAGATGAAGCTGTAATACTTGTGAAAGAAAACCTCACTGAAATTTCA	1619
Qy	2508	-----TGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCAC---CTCAGGAG	2559
Db	1620		
Qy	2508	TCTGAGTCAATGACAGGACATGACAATAAGGGAAACTCAGTGCTTCACCATCACCTGAG	1679
Qy	2560	CTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---T	2616
Db	1680		
Qy	2560	GGAGGAAAACCGTATTTGGAGTCTTTTCAGCCAGTTTAGGCATCACAAAAGATACCTTA	1739
Qy	2617	GCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAG	2676
Db	1740		
Qy	2617	GCACCTGATGAAGTTTCAGCATTGACCAAAAAGGAGAAAATCCCTTTGCAGATGGAGGAG	1799
Qy	2677	TTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAA	2736
Db	1800		
Qy	2677	CTCAATACTGCAGTTTATTCAAGTGATGGCTTATTCATTGCTCAGGAAGCAAACCTAAGA	1859
Qy	2737	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTT	2796
Db	1860		
Qy	2737	GAAAGTGAAACATTTTCAGATTTCATCTCCGATTGAGATTATAGATGAGTTCCCGACCTTT	1919
Qy	2797	GTCAGTGCTAA--AGATGATTCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTA	2853
Db	1920		
Qy	2797	GTCAGTTCTAAAGCAGATTCTTCTCCTACATTAGCCAGGGAATACACTGACCTAGAAGTA	1979
Qy	2854	TCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAA	2913
Db	1980		
Qy	2854	GCCCACAAAAGTGAAATTGCTGACATCCAGGATGGAGCTGGGTTCATTGGCTTGTGCAGGA	2039
Qy	2914	TTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAGTACATGTTTCAGAT	2973
Db	2040		
Qy	2914	TTGCCCCATGACCTTTCTTTCAAGAGTATACAACCTAAAGAGGAAGTTCATGTCCAGAT	2099
Qy	2974	GAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCT	3033
Db	2100		
Qy	2974	GAGTTCTCCAAGATAGGGGTGATGTTTCAAAGGTGCCCCGACTGCCTCCAGATGTTTCT	2159
Qy	3034	GCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAA	3093
Db	2160		
Qy	3034	GCTTTGGATGCTCAAGCAGAGATAGGCAGCATAGAAAAACCCAAAGTTCTTGTGAAAGAA	2219
Qy	3094	GCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTATTG	3153
Db	2220		
Qy	3094	GCCGAGAGAAAACTTCCTTCTGATACAGAAAAAGAGCGAAGATCTCCATCTGCTATATTT	2279
Qy	3154	TCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	3213

Db	2280	TCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAG	2339
Qy	3214	ACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATT	3273
Db	2340	ACTGGAGTGGTGTGTTGGTGCCAGCTTGTTCCTGCTGCTCTCGCTGACAGTATTCAGCATT	2399
Qy	3274	GTCAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATA	3333
Db	2400	GTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATA	2459
Qy	3334	TATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATAT	3393
Db	2460	TATAAGGGTGTGATCCAGGCTATCCAGAAATCTGATGAAGGCCACCCATTTCAGGGCATAT	2519
Qy	3394	TTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTT	3453
Db	2520	TTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGCAATTCTGCTCTT	2579
Qy	3454	GGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTT	3513
Db	2580	GGTCATGTTAACTGCACAATAAAAGAACTCAGACGCCTCTTCTTAGTTGATGATTTAGTT	2639
Qy	3514	GATTCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAAT	3573
Db	2640	GATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTCAAT	2699
Qy	3574	GGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAA	3633
Db	2700	GGTCTGACACTACTAATTTTGGCTCTGATTTCACTCTTCAGTGTTCCTGTTATTTATGAA	2759
Qy	3634	CGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCC	3693
Db	2760	CGGCATCAGGCGCAAATAGATCATTATCTGGGACTTGCAAATAAGAATGTTAAAGATGCT	2819
Qy	3694	ATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740
Db	2820	ATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGTAAAGCTGA	2866

RESULT 14

AAV30920

ID AAV30920 standard; cDNA; 2386 BP.

XX

AC AAV30920;

XX

DT 14-SEP-1998 (first entry)

XX

DE Human secreted protein BG160_1 cDNA.

XX

KW BG160_1; secreted protein; protein factor; human; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 102..2030

FT /*tag= a

FT sig_peptide 1863. .1899
 FT /*tag= b
 FT /note= "putative leader/signal peptide"
 FT mat_peptide 1900. .2027
 FT /*tag= c
 XX
 PN WO9817687-A2.
 XX
 PD 30-APR-1998.
 XX
 PF 24-OCT-1997; 97WO-US019590.
 XX
 PR 25-OCT-1996; 96US-00740274.
 PR 24-OCT-1997; 97US-00740274.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Jacobs K, Mccoy JM, Lavallie ER, Racie LA, Merberg D, Treacy M;
 PI Spaulding V, Agostino MJ;
 XX
 DR WPI; 1998-261426/23.
 DR P-PSDB; AAW58383.
 XX
 PT Nucleic acid encoding secreted protein from human cells - useful, e.g. as
 PT immuno-modulators, anti-tumour agents, promoters of tissue growth,
 PT haemostatic and thrombolytic agents etc.
 XX
 PS Claim 20; Page 74-75; 114pp; English.
 XX
 CC This cDNA clone, designated BGL60_1, codes for a novel human secreted
 CC protein (see AAW58383). It was isolated from a human adult brain cDNA
 CC library using methods selective for cDNAs that encode secreted proteins.
 CC The clone is deposited in composite clone ATCC 98232; an oligonucleotide
 CC (see AAT99725) is designed to isolate the clone from the composite. The
 CC predicted AT415_4 amino acid sequence shows homology to neuroendocrine-
 CC specific proteins. Novel cDNA clones (see AAV30916-32) coding for human
 CC secreted proteins (see AAW58580-90) are claimed. These can be used for
 CC recombinant production of the secreted proteins for analysis,
 CC characterisation, diagnostic or therapeutic use. They can also be used as
 CC tissue or mol.wt. markers, for chromosome identification, to identify
 CC genetic disorders, to isolate new related DNA, as sources of primers for
 CC PCR, to generate antibodies, and in interaction trap assays. The secreted
 CC proteins may also have many biological activities, e.g. cytokine,
 CC immunomodulator, haematopoiesis regulating activity, tissue growth
 CC activity, activin or inhibin activity, chemotactic or chemokinetic
 CC activity, haemostatic and thrombolytic activity, receptor/ligand
 CC activity, antiinflammatory, cadherin and tumour invasion suppressor
 CC activity, and tumour inhibition activity. The proteins can be expressed
 CC in vivo from DNA, introduced in gene therapy vectors
 XX
 SQ Sequence 2386 BP; 756 A; 450 C; 494 G; 686 T; 0 U; 0 Other;

Query Match 37.7%; Score 1411.2; DB 2; Length 2386;
 Best Local Similarity 83.3%; Pred. No. 5e-288;
 Matches 1702; Conservative 0; Mismatches 303; Indels 39; Gaps 7;

Qy 1718 CCAAAACGTCAAATCCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAA 1777

Db	1	CCAAAACATCAAACCCCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAA	60
Qy	1778	CAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGC	1837
Db	61	CAGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTC	120
Qy	1838	CAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTG	1897
Db	121	CAGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTG	180
Qy	1898	CTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACC	1957
Db	181	CTTATGAAACAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATC	240
Qy	1958	CCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGC	2017
Db	241	CTGCAGCACAGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGC	300
Qy	2018	CTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAG	2077
Db	301	CTGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGA	360
Qy	2078	TGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGC	2137
Db	361	TACAGCCCAGCTCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAAC	417
Qy	2138	TTGAGCCTGAAAACCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTT	2194
Db	418	ATGAGCCTGAAAACCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTAT	477
Qy	2195	TGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAG	2254
Db	478	CAGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAG	537
Qy	2255	AAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGC	2314
Db	538	AAGCTCCTTATATATCTATTGCGTGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAAC	597
Qy	2315	CAAGTCCAGATTTCTCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAAC	2374
Db	598	CAGCTCCGATTTCTCTGATTATTCAGAAATGGCAAAGTTGAACAGCCAGTGCCTGATC	657
Qy	2375	ACGCTGAGCTAGTGGAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATG	2434
Db	658	ATTCTGAGCTAGTTGAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATG	717
Qy	2435	ATTCGATTCCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTC	2494
Db	718	ATTCAATACCTGACGTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTC	777
Qy	2495	TCACTGA-----AGTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCT	2548
Db	778	TCACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTT	837
Qy	2549	CACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAA	2608

Db		838 TGCCACCTGAGGGAGGAAAGCCATATTTTGAATCTTTTAAGCTCAGTTTTAGATAAACACAA	897
Qy	2609 AAGATGC---	TGCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGC	2665
Db		898 AAGATACCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGC	957
Qy	2666 AAATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAG	2725	
Db		958 AGATGGAGGAGCTCAGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAG	1017
Qy	2726 ACAAAATAAAAGAAAGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAAT	2785	
Db		1018 CACAGATAAGAGAAACTGAAACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGT	1077
Qy	2786 TTCCCACGTTTGTGCTGCTAAAGATGATTC---	TCCTAAATTAGCCAAGGAGTACACTG	2842
Db		1078 TCCCTACATTGATCAGTTCATAAACTGATTCATTTCTAAATTAGCCAGGGAATATACTG	1137
Qy	2843 ATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGC	2902	
Db		1138 ACCTAGAAGTATCCACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGC	1197
Qy	2903 CTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG---	2959	
Db		1198 CTTGCACAGAATTGCCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGA	1257
Qy	2960 ---TACATGTTTCAGATGAATTCCTCGAAAATAGGTCCAGTGTATCTAAGGCATCCATAT	3016	
Db		1258 AAATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTAT	1317
Qy	3017 CGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCA	3076	
Db		1318 TGCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCA	1377
Qy	3077 AATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGAT	3136	
Db		1378 AAGTTCTTGTGAAAGAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGAT	1437
Qy	3137 CCCTGTGACGTGTATTGTCAGCAGAGCTGAGTAAAAC TTCAGTTGTTGACCTCCTCTACT	3196	
Db		1438 CACCATCTGCTATATTTTCAGCAGAGCTGAGTAAAAC TTCAGTTGTTGACCTCCTGTACT	1497
Qy	3197 GGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGTGCCAGCTTATTCCTGCTGCTGTCTC	3256	
Db		1498 GGAGAGACATTAAGAAGACTGGAGTGGTGTGGTGGTGCCAGCCTATTCCTGCTGCTTTTCAT	1557
Qy	3257 TGACAGTGTTTCAGCATTGTCAGTGTAACGGCTACATTGCCTTGGCCCTGCTCTCGGTGA	3316	
Db		1558 TGACAGTATTCAGCATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGA	1617
Qy	3317 CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC	3376	
Db		1618 CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC	1677
Qy	3377 ACCCATTACAGGCGATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAAT	3436	
Db		1678 ACCCATTACAG-----GAAGTTGCTATATCTGAGGAGTTGGTTTCAGAAAT	1722

Qy 3437 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCT 3496
 |||
 Db 1723 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAAGAACTGAGGCGGCTTTTCT 1782
 Qy 3497 TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATG 3556
 |||
 Db 1783 TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATG 1842
 Qy 3557 TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA 3616
 |||
 Db 1843 TTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTG 1902
 Qy 3617 TTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACA 3676
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 Db 1903 TTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA 1962
 Qy 3677 AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3736
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 Db 1963 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 2022
 Qy 3737 CAGA 3740
 ||
 Db 2023 CTGA 2026

RESULT 15

AAF98399

ID AAF98399 standard; cDNA; 2386 BP.

XX

AC AAF98399;

XX

DT 07-JUN-2001 (first entry)

XX

DE Human cDNA clone BG160_1 sequence SEQ ID 41.

XX

KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
 KW differentiation; immune system modulator; tissue growth; chemotactic;
 KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
 KW haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO200119988-A1.

XX

PD 22-MAR-2001.

XX

PF 14-SEP-2000; 2000WO-US025135.

XX

PR 17-SEP-1999; 99US-00398829.

XX

PA (GEMY) GENETICS INST INC.

XX

PI Jacobs K, Mccoy JM, Lavallie ER, Collins-Racie LA, Evans C;

PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;

XX

DR WPI; 2001-244801/25.

DR P-PSDB; AAB90682.
 XX
 PT Isolated nucleic acids encoding polypeptides, useful for modulating e.g.
 PT cytokine and cell proliferation/differentiation activity, the immune
 PT system and hematopoiesis regulating activity.
 XX
 PS Claim 1; Page 408-409; 557pp; English.
 XX
 CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
 CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
 CC tissue types, and may be used in the prevention, treatment and diagnosis
 CC of diseases associated with inappropriate protein expression. The
 CC polypeptides and nucleic acids may be used as nutrients or to modulate
 CC cytokine and cell proliferation/differentiation activity and may also be
 CC involved in modulation of the immune system. The cDNA sequences,
 CC proteins, their agonists and/or antagonists exhibit haematopoiesis
 CC regulating activity; tissue growth activity; activin/inhibin activity;
 CC chemotactic/chemokinetic activity; haemostatic and thrombolytic activity;
 CC receptor/ligand activity; anti-inflammatory activity; haematopoiesis
 CC activity; cadherin/tumour suppressor activity; and/or tumour inhibition
 CC activity. Included in the invention are probes represented in AAF98490 -
 CC AAF98572 which are specific for the cDNA clones encoding the secreted
 CC proteins
 XX
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Query Match 37.6%; Score 1408; DB 5; Length 2386;
 Best Local Similarity 83.2%; Pred. No. 2.4e-287;
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Qy	1778	CAGATACCTTATCAAAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGC	1837
Db	61	CAGATAATTTAACAAAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTC	120
Qy	1838	CAGATTTAGTTCAGGAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTG	1897
Db	121	CAGATTTAGTACAGGAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTG	180
Qy	1898	CTTATGAAACAAAAGTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACC	1957
Db	181	CTTATGAAACAAAATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATC	240
Qy	1958	CCACAGCACAGCTTTGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGC	2017
Db	241	CTGCAGCACAGCTTTGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGC	300
Qy	2018	CTGATATTGTTATGGAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAG	2077
Db	301	CTGACATTGTTATGGAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGA	360
Qy	2078	TGCAGCCCAGTGTATCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGC	2137
Db	361	TACAGCCCAGCTCATCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAAC	417

Qy	2138	TTGAGCCTGAAAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTT	2194
Db	418	ATGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTAT	477
Qy	2195	TGGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAG	2254
Db	478	CAGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAG	537
Qy	2255	AAGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGC	2314
Db	538	AAGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAAC	597
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Qy	2726	ACAAAATAAAAGAAAGTGAACATTTTCAGATTCACTCCGATTGAGATAATAGATGAAT	2785
Db	1018	CACAGATAAGAGAAACTGAAACGTTTTTCAGATTCACTCCAATTGAAATTATAGATGAGT	1077
Qy	2786	TTCCACGTTTGTGAGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTG	2842
Db	1078	TCCCTACATTGATCAGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTG	1137
Qy	2843	ATCTAGAAGTATCCGACAAAAGTGAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGC	2902
Db	1138	ACCTAGAAGTATCCACAAAAGTGAATTGCTAATGCCCCGGATGGAGCTGGGTCAATTGC	1197
Qy	2903	CTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG---	2959
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Qy	3077	AATCACTTACGAAAGAAGCAGAGAAAAAATTCCTTCTGACACAGAGAAAGAGGACAGAT	3136
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Qy	3137	CCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAATTCAGTTGTTGACCTCCTCTACT	3196
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Db	1498	GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCAT	1557
Qy	3257	TGACAGTGTTTCAGCATTGTTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGA	3316
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Qy	3317	CTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCC	3376
Db	1618	CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC	1677
Qy	3377	ACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAAT	3436
Db	1678	ACCCATTTCAGG-----GAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGT	1722
Qy	3437	ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAATAAAGAACTGAGGCGGCTTTTCT	3496
Db	1723	ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAAGGAATCAGGCGCCTCTTCT	1782
Qy	3497	TAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATG	3556
Db	1783	TAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATG	1842
Qy	3557	TTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTA	3616
Db	1843	TTGGTGCCTTGTTTAAATGGTCTGACACTACTGATTTTGGCTCTCATTTCCTCCTCAGTG	1902
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Db	1903	TTGGTGTATTTATGAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATA	1962
Qy	3677	AGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG	3736
Db	1963	AGAATGTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG	2022
Qy	3737	CAGA 3740	
Db	2023	CTGA 2026	

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Job time : 1328.89 secs

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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 01:30:35 ; Search time 232.145 Seconds
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Perfect score: 3741
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2323.8	62.1	4822	4	US-09-484-970B-106	Sequence 106, App
2	497.4	13.3	799	2	US-08-700-607-2	Sequence 2, Appli
3	484.8	13.0	2610	4	US-09-023-655-382	Sequence 382, App
4	228.8	6.1	1766	4	US-09-149-476-254	Sequence 254, App
5	228.8	6.1	2664	4	US-09-149-476-255	Sequence 255, App
6	203.6	5.4	1095	2	US-08-700-607-4	Sequence 4, Appli
7	198	5.3	454	4	US-09-621-976-740	Sequence 740, App
8	196.6	5.3	463	4	US-09-621-976-741	Sequence 741, App
9	180.4	4.8	794	4	US-09-149-476-102	Sequence 102, App
10	164.6	4.4	261	2	US-08-700-607-9	Sequence 9, Appli
c 11	75.4	2.0	7218	1	US-08-232-463-14	Sequence 14, Appl

	12	75.2	2.0	152331	3	US-09-128-155-16	Sequence 16, Appl
c	13	74.6	2.0	2481	4	US-09-894-998A-35	Sequence 35, Appl
c	14	73.2	2.0	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	15	73.2	2.0	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	16	71.8	1.9	1614	4	US-09-616-289-45	Sequence 45, Appl
	17	71.8	1.9	12425	4	US-09-616-289-50	Sequence 50, Appl
c	18	68.6	1.8	319	3	US-09-165-264-8	Sequence 8, Appli
	19	68	1.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
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c	21	67.8	1.8	320	3	US-09-165-264-13	Sequence 13, Appl
c	22	67.6	1.8	320	3	US-09-165-264-7	Sequence 7, Appli
	23	67.6	1.8	15378	3	US-08-785-420-1	Sequence 1, Appli
c	24	67.4	1.8	4600	4	US-09-702-705-1797	Sequence 1797, Ap
c	25	67.4	1.8	4600	4	US-09-736-457-1797	Sequence 1797, Ap
c	26	67.4	1.8	4600	4	US-09-671-325-1797	Sequence 1797, Ap
c	27	66.8	1.8	320	3	US-09-165-264-11	Sequence 11, Appl
c	28	65.8	1.8	320	3	US-09-165-264-14	Sequence 14, Appl
	29	65.4	1.7	2561	4	US-09-616-289-48	Sequence 48, Appl
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	34	63.6	1.7	4041	3	US-09-105-537-36	Sequence 36, Appl
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	36	63.6	1.7	38506	3	US-09-320-878-19	Sequence 19, Appl
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	38	63.6	1.7	38506	4	US-09-657-440-19	Sequence 19, Appl
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c	45	60.6	1.6	12001	1	US-08-458-568A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1

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US-09-484-970B-106
; Sequence 106, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.
; APPLICANT: Volkmuth, Wayne
; APPLICANT: Walker, Michael G.
; TITLE OF INVENTION: BONE REMODELING GENES
; FILE REFERENCE: PB-0014 US
; CURRENT APPLICATION NUMBER: US/09/484,970B
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PERL Program
; SEQ ID NO 106
; LENGTH: 4822
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6426186 444857.15CB1
; NAME/KEY: unsure
; LOCATION: 33, 51, 79, 211, 369, 483-484, 731, 748, 4803, 4805-4806, 4808-4809,
; OTHER INFORMATION: a, t, c, g, or other
US-09-484-970B-106
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Query Match          62.1%; Score 2323.8; DB 4; Length 4822;
Best Local Similarity 80.9%; Pred. No. 0;
Matches 3060; Conservative 0; Mismatches 587; Indels 137; Gaps 25;
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Qy      63 CGCGAAGGCAGCAGAAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCG 122
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Db      78 CNCGGAGGCAGGAGGAGCAGTCTCATTGTTCCGGGAGCCGTCACCACAGTAGGTCCCTCG 137

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Qy     242 ACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCC 301
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy     302 CGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCCGAGGACGAGGAGG 361
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     299 CACCCCGGCCGAGCCCCGCTTCAAGTACCAGTTCGTGAGGGAGCCCCGAGGACGAGGAG- 357

Qy     362 ACGAGGAGGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACCTGGAGGTGC 421
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     358 --GAAGAAGAGGANGATGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGC 415

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Qy     476 CCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGGCCGCTGC 535
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy	2139	TGAGCCTGAAAACCCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTT	2195
Db	2207	TGAGCCTGAAAACCCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATC	2266
Qy	2196	GGGAACAAAGGAAGGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGA	2255
Db	2267	AGGAATAAAGGAAGAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGA	2326
Qy	2256	AGCTCCTTATATATCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCC	2315
Db	2327	AGCTCCTTATATATCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACC	2386
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Db		2387 AGCTCCGGATTTTCTCTGATTATTTCAGAAATGGCAAAAAGTTGAACAGCCAGTGCCCTGATCA	2446
Qy		2376 CGCTGAGCTAGTGGAGGATTTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGA	2435
Db		2447 TTCTGAGCTAGTTGAAGATTTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGA	2506
Qy		2436 TTCGATTCTCTGAAGTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCT	2495
Db		2507 TTCAATACTGACGTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCT	2566
Qy		2496 CACTGA-----AGTGTCTGAGACAGTAGCCCGCACAAGAGGAGAGACTTAGTGCCTC	2549
Db		2567 CACTGAGACTTCATTTGAGTCAATGATAGAATATGAAAATAAGGAAAAAAGTCTAGTGCTTT	2626
Qy		2550 ACCTCAGGAGCTAGGAAAGCCATATTTAGAGTCTTTTTAGGCCCAATTTACATAGTACAAA	2609
Db		2627 GCCACCTGAGGGAGGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAA	2686
Qy		2610 AGATGC---TGCATCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCA	2666
Db		2687 AGATACCCTGTTACCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCA	2746
Qy		2667 AATGGAAGAGTTTAATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGA	2726
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Qy		2727 CAAAATAAAAGAAAGTGAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATT	2786
Db		2807 ACAGATAAGAGAAACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTT	2866
Qy		2787 TCCCACGTTTGTGCTAGTCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGA	2843
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Qy		2844 TCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATCCAAAGCGGGGAGATTTCATTGCC	2903
Db		2927 CCTAGAAGTATCCCACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCTATTGCC	2986
Qy		2904 TTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG----	2959
Db		2987 TTGCACAGAATTGCCCCATGACCTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAA	3046
Qy		2960 --TACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGATCTAAGGCATCCATATC	3017
Db		3047 AATCAGTTTCTCAGATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATT	3106
Qy		3018 GCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAA	3077
Db		3107 GCCTCCAGATGTTTCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAA	3166
Qy		3078 ATCACTTACGAAAGAAGCAGAGAAAAAACTTCTTCTGACACAGAGAAAGAGGACAGATC	3137
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Qy 3197 GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTC 3256
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 Db 3287 GGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCA 3346
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 Db 3407 CCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCC 3466
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 Db 3467 ACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTTCAAGAA 3526
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 Db 3527 ACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCT 3586
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 Db 3767 AGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAG 3826
 Qy 3737 CAGA 3740
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 Db 3827 CTGA 3830

RESULT 2

US-08-700-607-2

; Sequence 2, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

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;      STATE:  CA
;      COUNTRY:  U.S.
;      ZIP:  94304
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/700,607
;      FILING DATE:  Filed Herewith
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0114 US
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      INFORMATION FOR SEQ ID NO:  2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  799 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  cDNA
;      IMMEDIATE SOURCE:
;      LIBRARY:
;      CLONE:  Consensus
US-08-700-607-2

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Query Match          13.3%;  Score 497.4;  DB 2;  Length 799;
Best Local Similarity 92.7%;  Pred. No. 1.4e-106;
Matches 522;  Conservative 0;  Mismatches 41;  Indels 0;  Gaps 0;

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Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
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Db      108 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 167

Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTGAGCATTGTGAGTGTAACGGCCTACATTGCC 3297
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Db      168 CTATTCCTGCTGCTTTTCATTGACAGTATTGAGCATTGTGAGCGTAACAGCCTACATTGCC 227

Qy      3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
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Db      228 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 287

Qy      3358 CAGAAATCAGATGAAGGCCACCCATTGAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
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Db      288 CAGAAATCAGATGAAGGCCACCCATTGAGGGCATATCTGGAATCTGAAGTTGCTATATCT 347

Qy      3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
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Db      348 GAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGTCATGTGAAGTGCACGATAAAG 407

Qy      3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
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Db      408 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 467

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Qy 3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
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 Qy 3598 CTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
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 Db 528 CTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 587
 Qy 3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
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 Db 588 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 647
 Qy 3718 CCTGGATTGAAGCGCAAAGCAGA 3740
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 Db 648 CCTGGATTGAAGCGCAAAGCTGA 670

RESULT 3

US-09-023-655-382

; Sequence 382, Application US/09023655

; Patent No. 6607879

; GENERAL INFORMATION:

; APPLICANT: Cocks, Benjamin G.

; APPLICANT: Susan G. Stuart

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 1508

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/023,655

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0001 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 382:

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; SEQUENCE CHARACTERISTICS:
;   LENGTH: 2610 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: LUNGNOT14
;   CLONE: 1508778
US-09-023-655-382

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Query Match          13.0%; Score 484.8; DB 4; Length 2610;
Best Local Similarity 92.4%; Pred. No. 2.4e-103;
Matches 521; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

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Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
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Db      1311 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 1370

Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTCAGTGTAAACGGCCTAC-ATTGC 3296
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Db      1371 CTATTCCTGCTGCTTTCATTGACAGTATTGAGCATTGTGAGCGTAACAGCCTACAATTGC 1430

Qy      3297 CTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTAT 3356
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Db      1431 CTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGGTGTGATCCAAGCTAT 1490

Qy      3357 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATC 3416
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Db      1491 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATC 1550

Qy      3417 AGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAA 3476
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RESULT 4
US-09-149-476-254

; Sequence 254, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
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; EARLIER APPLICATION NUMBER: 60/056,903
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; EARLIER APPLICATION NUMBER: 60/056,894
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; EARLIER APPLICATION NUMBER: 60/056,845
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; EARLIER APPLICATION NUMBER: 60/047,595
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632

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; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,876
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; EARLIER APPLICATION NUMBER: 60/056,881
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; EARLIER APPLICATION NUMBER: 60/056,909
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; EARLIER APPLICATION NUMBER: 60/056,875
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; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          6.1%;  Score 228.8;  DB 4;  Length 1766;
Best Local Similarity 63.4%;  Pred. No. 1.3e-43;
Matches 350;  Conservative 0;  Mismatches 202;  Indels 0;  Gaps 0;

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Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGC 3233
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Db      286  TGCGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 345

Qy      3234 CAGCTTATTCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAACGGCCTACAT 3293
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Db      346  CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCATCAGTGTTGTTTCTTACCT 405

Qy      3294 TGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGC 3353
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Db      406  CATCCTGGCTCTTCTCTCTGTCAACATCAGCTTCAGGATCTACAAGTCCGTATCCAAGC 465

Qy      3354 TATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTAT 3413
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Qy      3414 ATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAAT 3473
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Qy      3474 AAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGT 3533
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Db      586  GAAACTCATTATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 645

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QY 3534 GTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTT 3593
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 QY 3594 AGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGA 3653
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 Db 706 TGCTGAAGTGTCTCATTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGA 765
 QY 3654 TCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAA 3713
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 Db 766 TCACTATGTTGGCATCGCCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAA 825
 QY 3714 AATCCCTGGATT 3725
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 Db 826 ACTCCCTGGAAT 837

RESULT 5

US-09-149-476-255

; Sequence 255, Application US/09149476
 ; Patent No. 6420526
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: PZ002P1
 ; CURRENT APPLICATION NUMBER: US/09/149,476
 ; CURRENT FILING DATE: 1998-09-08
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493
 ; EARLIER FILING DATE: 1998-03-06
 ; EARLIER APPLICATION NUMBER: 60/040,162
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/040,333
 ; EARLIER FILING DATE: 1997-03-07
 ; EARLIER APPLICATION NUMBER: 60/038,621
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 ; EARLIER FILING DATE: 1997-05-23
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 ; EARLIER FILING DATE: 1997-05-23
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 ; EARLIER APPLICATION NUMBER: 60/047,502
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; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/047,586

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; EARLIER APPLICATION NUMBER: 60/057,650
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; EARLIER APPLICATION NUMBER: 60/056,884
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; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

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Query Match          6.1%;  Score 228.8;  DB 4;  Length 2664;
Best Local Similarity 63.4%;  Pred. No. 1.6e-43;
Matches 350;  Conservative 0;  Mismatches 202;  Indels 0;  Gaps 0;

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Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGTC 3233
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Db      261  TCGGGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 320

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Qy 3234 CAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACAT 3293
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 Db 321 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTATCAGTGTGGTTTCTTACCT 380
 Qy 3294 TGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGC 3353
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 Db 381 CATCCTGGCTCTTCTCTCTGTACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 440
 Qy 3354 TATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCTAT 3413
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 Db 441 TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 500
 Qy 3414 ATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAAT 3473
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 Db 501 GTCCTCAGAAGCTTTCATAATTACATGAATGCTGCCATGGTGACATCAACAGGGCCCT 560
 Qy 3474 AAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGAGT 3533
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 Db 561 GAAACTCATTATTTCGTCTCTTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCTGT 620
 Qy 3534 GTTGATGTGGGTGTTTACTTATGTTGGTGCCCTTGTTCATGGTCTGACACTACTGATTTT 3593
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 Db 621 CTTTATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCTTCTAATTCT 680
 Qy 3594 AGCTCTGATCTCACTCTTCAGTATTCTCTGTTATTTATGAACGGCATCAGGTGCAGATAGA 3653
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 Db 681 TGCTGAACTGCTCATTTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATTGA 740
 Qy 3654 TCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAA 3713
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 Db 741 TCACTATGTTGGCATCGCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCAAGCAAA 800
 Qy 3714 AATCCCTGGATT 3725
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 Db 801 ACTCCCTGGAAT 812

RESULT 6

US-08-700-607-4

; Sequence 4, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1095 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: THPINOB01
; CLONE: 31870
US-08-700-607-4

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Query Match          5.4%; Score 203.6; DB 2; Length 1095;
Best Local Similarity 61.6%; Pred. No. 7.6e-38;
Matches 337; Conservative 1; Mismatches 208; Indels 1; Gaps 1;

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Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGTC 3233
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Db      328  TGCGGTGCACGATCTGATTTTMTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTGGCAC 387

Qy      3234 CAGCTTATTCTGCTGCTGTCTCTGACAGTGTTGAGCATTGTCAGTGTAACGGCCTACAT 3293
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Db      388  CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTTCAGTGTCATCAGTGTTGTTTCTTACCT 447

Qy      3294 TGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGC 3353
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Db      448  CATCCTGGCTCTTCTCTCTGTCAACCATCAGCTTCAGGATCTACAAGTCCGTCATCCAAGC 507

Qy      3354 TATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTAT 3413
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Db      508  TGTACAGAAGTCAGAAGAAGGCCATCCATTCAAAGCCTACCTGGACGTAGACATTACTCT 567

Qy      3414 ATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAAT 3473
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Db      688  CTTTCATGTGGCTGATGACCTATGTTGGTGCTGTTTTTAACGGAATCACCCCTTCTAATTCT 747

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Qy 3594 AGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGA 3653
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Qy 3714 AATCCCT 3720
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 Db 867 AGTTACT 873

RESULT 7

US-09-621-976-740
 ; Sequence 740, Application US/09621976
 ; Patent No. 6639063
 ; GENERAL INFORMATION:
 ; APPLICANT: Dumas Milne Edwards, J.B.
 ; APPLICANT: Jobert, S.
 ; APPLICANT: Giordano, J.Y.
 ; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 ; FILE REFERENCE: GENSET.054PR2
 ; CURRENT APPLICATION NUMBER: US/09/621,976
 ; CURRENT FILING DATE: 2000-07-21
 ; NUMBER OF SEQ ID NOS: 19335
 ; SOFTWARE: Patent.pm
 ; SEQ ID NO 740
 ; LENGTH: 454
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 229..453
 US-09-621-976-740

Query Match 5.3%; Score 198; DB 4; Length 454;
 Best Local Similarity 71.8%; Pred. No. 9.5e-37;
 Matches 359; Conservative 7; Mismatches 72; Indels 62; Gaps 6;

Qy 19 GGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAGCAGAA 78
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Qy 79 GCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGGCACGA 138
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Qy 139 CTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACTCTGAG 198
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 Db 175 ACGCGGCCCCGGCGGCGGCGGCGAGCAGCTGCAGCATCATC-TCCACCCTCCAGCCATGGA 233

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Qy      258 AGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGCCCTCCGCC 317
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Qy      318 CGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGGAGGA 377
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Qy      378 GGACGAGGAGGAGGACGACGAGGACCTAGAGGAACCTGGAGGTGCTGGAGAGGAAGCCCGC 437
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Qy      438 AGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCCGCTGCTGGA 491
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RESULT 8

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US-09-621-976-741
; Sequence 741, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 741
; LENGTH: 463
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 237..461
; NAME/KEY: misc_feature
; LOCATION: 20
; OTHER INFORMATION: n=a, g, c or t
US-09-621-976-741

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Query Match          5.3%; Score 196.6; DB 4; Length 463;
Best Local Similarity 70.2%; Pred. No. 2e-36;
Matches 358; Conservative 12; Mismatches 78; Indels 62; Gaps 6;

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Qy      10 CTGGGCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAG 69
      || | : :: : |||| | ||||| ||||| |||| | |||| |
Db      9 CTCATCTRGBRNRGCGGCGGCAAGTGGGGACAGGGCGGGTGGCGCATCACCGGCGCGGAG 68

Qy      70 GCAGCAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGTTCTTCGGCTCGGC 129
      |||| || ||||| ||||| ||||| ||||| |||| | |||| | ||||

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Db          69 GCAGGAGGAGCAGTCTCATTGTTCCGGGAGCCGTCACCACAGTAGGTCCCTCGG----- 122
Qy          130 TCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCCGC 189
              ||| | | ||| ||||| ||||| | ||||| ||||| ||||| |||||
Db          123 -----CTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCCGC 173
Qy          190 GACTCTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCC 248
              | ||||| | | | | | ||||| | ||||| ||||| | | ||| | |
Db          174 GGCTCTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCCTCC 232
Qy          249 AGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCG 308
              ||||| ||||| | ||||| | ||||| ||||| ||||| |||||
Db          233 AGCCATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCCTCGGACAGCCACCCCG 289
Qy          309 GCCTCCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGA 368
              ||: | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          290 GCMGCAGCCCGCGTTCAAGTACCAGTTCRTGAGGGAGCCCGAGGACGAGGAG----- 341
Qy          369 GGAGGAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAG 428
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Db          342 -----GAAGACCTGGAGGAGCTGGAGGTGCTGGAGAG 373
Qy          429 GAAGCCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCCGCC 482
              ||||| |||||: ||: |||||: ||| || | |||| | || ||: ||: | |||||
Db          374 GAAGCCCGCMGCMGGGCTGTMCGCGGCCCCAGTGCMCACMGCMCTGCMGCMGGCGCGCC 433
Qy          483 GCTGCTGGACTTCAGCAGCGACTCGGTGCC 512
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Db          434 CCTGATGGACTTCGGAAATGACTTCGTGCM 463

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RESULT 9

US-09-149-476-102

; Sequence 102, Application US/09149476

; Patent No. 6420526

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P1

; CURRENT APPLICATION NUMBER: US/09/149,476

; CURRENT FILING DATE: 1998-09-08

; EARLIER APPLICATION NUMBER: PCT/US98/04493

; EARLIER FILING DATE: 1998-03-06

; EARLIER APPLICATION NUMBER: 60/040,162

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,333

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/038,621

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,626

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,334

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,336

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/040,163

; EARLIER FILING DATE: 1997-03-07

; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674

; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
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; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,894
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; EARLIER APPLICATION NUMBER: 60/056,911
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; EARLIER APPLICATION NUMBER: 60/056,636
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; EARLIER APPLICATION NUMBER: 60/056,910
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,864
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,631
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,845
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,892
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,761
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/047,595
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,599
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,588
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,585
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,586
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,590
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,594
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669

; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 4.8%; Score 180.4; DB 4; Length 794;
Best Local Similarity 61.0%; Pred. No. 1.7e-32;
Matches 332; Conservative 6; Mismatches 202; Indels 4; Gaps 3;

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Qy      3174 TTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGC 3233
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Db      253 TGCAGTGCACGATCTGATTTTCTGGAGAGATGTGAAGAAGACTGGGTTTGTCTTTG--GA 310

Qy      3234 CAGCTTATTCTGCTGCTGTCTCTGACAGTGTTGAGCATTGTCAGTGTAACGGCC--TACA 3292
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      311 CACGCTGATCATGCTGCTTTCCCTGGCAGCTTTCAGTGTCTCATCARTGTGGGTTTCTTAMC 370

Qy      3293 TTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGG 3352
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      371 TCATCCTGGCTCTTCTCTCTGTCAACCATCARCTTCAGGATCTACAAGTCCGTCATCCAAG 430

Qy      3353 CTATCCAGAAATCAGATGAAGGCCACCCATT--CAGGGCATATTTAGAATCTGAAGTTGCT 3411
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      431 CTGTWCAGAARTCAGAAARAAGGCCATCCAWTCCAAAGCCTACCTGGACGTAGACATTACT 490

Qy      3412 ATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACA 3471
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      491 CTGTCCTCAGAAGCTTTCCATAATTACATGAATGCTGCCATGGTGCACATCAACAGGGGCC 550

Qy      3472 ATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCA 3531
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      551 CTGAAACTCATTATTTCGTCTCTTCTGGTAGAAGATCTGGTTGACTCCTTGAAGCTGGCT 610

Qy      3532 GTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATT 3591
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      611 GTCTTCATGTGGCTGATGACCTATGTTGGTGTCTGTTTTTAACGGAATCACCCCTTCTAATT 670

Qy      3592 TTAGCTCTGATCTCACTCTTCAGTATTCTGTTATTTATGAACGGCATCAGGTGCAGATA 3651
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      671 CTTGCTGAACTGCTCATTTTTCAGTGTCCCGATTGTCTATGAGAAGTACAAGACCCAGATT 730

Qy      3652 GATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCA 3711
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      731 GATCACTATGTTGGCATCGCCCGAGATCAGACCAAGTCAATTGTTGAAAAGATCCCAAGC 790

Qy      3712 AAAA 3715
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Db      791 AAAA 794
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RESULT 10

US-08-700-607-9

; Sequence 9, Application US/08700607
; Patent No. 5858708
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga

```

; APPLICANT: Au-Young, Janice
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 261 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: SPLNFET01
; CLONE: 28742
US-08-700-607-9

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Query Match          4.4%; Score 164.6; DB 2; Length 261;
Best Local Similarity 86.7%; Pred. No. 4.4e-29;
Matches 176; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Qy      3237 CTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAACGGCCTACATTGC 3296
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Db      1 CCTATNCCNGCTGCTTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGC 60

Qy      3297 CTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTAT 3356
          ||| ||||| ||| |||| ||||| |||| |||| |||| ||||| |||||
Db      61 CTTNGCCCTGCNCTCTGTGACCATCAGCTNTAGGCTATACAAGGGTGTGATCCAAGCTAT 120

Qy      3357 CCAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATC 3416
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121 CCAGAAATCAGATGAAGGNCACCCATTCAGGGCATATCTGGANTCTGAAGTTGCTATATC 180

Qy      3417 AGAGGAATTGGTTCAGAAATACA 3439
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Db 181 TGAGGAGTTGNTTCAGAAGTACA 203

RESULT 11

US-08-232-463-14/c

; Sequence 14, Application US/08232463

; Patent No. 5670367

; GENERAL INFORMATION:

; APPLICANT: DORNER, F.

; APPLICANT: SCHEIFLINGER, F.

; APPLICANT: FALKNER, F. G.

; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

; NUMBER OF SEQUENCES: 52

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 1800 Diagonal Road, Suite 500

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22313-0299

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/232,463

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/935,313

; FILING DATE:

; APPLICATION NUMBER: EP 91 114 300.6

; FILING DATE: 26-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 30472/114 IMMU

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703)836-9300

; TELEFAX: (703)683-4109

; TELEX: 899149

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7218 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; CLONE: pTZgpt-F1s

US-08-232-463-14

Query Match 2.0%; Score 75.4; DB 1; Length 7218;

Best Local Similarity 5.3%; Pred. No. 1.9e-07;

Matches 22; Conservative 242; Mismatches 153; Indels 0; Gaps 0;

Qy 1127 TTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAA 1186

[illegible]

US-09-128-155-16

; Patent No. 6117654

; GENERAL INFORMATION:

; APPLICANT: Pan, Yang

7 TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: 09404/052001

; CURRENT APPLICATION NUMBER: US/09/128,155

; CURRENT FILING DATE: 1998-08-03

; EARLIER APPLICATION NUMBER: US 60/091,650

; EARLIER FILING DATE: 1998-07-02

; EARLIER APPLICATION NUMBER: US 60/054,646

; EARLIER FILING DATE: 1997-08-04

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; NUMBER OF SEQ ID NOS: 18
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; SOFTWARE: FastSEQ for Windows Version 3.0
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; SEQ ID NO 16

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; LENGTH: 152331
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; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

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; NAME/KEY: misc feature
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; LOCATION: (1)...(152331)
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; OTHER INFORMATION: n = A,T,C or G

US-09-128-155-16

Query Match 2.0%; Score 75.2; DB 3; Length 152331;
Best Local Similarity 53.8%; Pred. No. 1.2e-06;

Matches 155; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

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Qy      463 CCGCCCCCGCCGCGCCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCC 522
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Db      21936 CCCCCCCCCCGGCGCGCCCCCGCGGCCCCCACCCCCCCCCCCCCCCCCCGCGCCC 21995

Qy      523 CGCGGGCGCTGCCGGCCGCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGC 582
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Db      21996 CGCCCCCCCCCGCGCCCCCACCCCCCGCCCCCGCCCCCCCCCCCCCCCCCAC 22055

Qy      583 AGCCCCGCGGCGCCGCGCCATCCCTGCCGCGCGCTGCCGAGTCCTGCCCTCCAAGCTC 642
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      22056 CCCCACACCGGCGCCACACGCACCCCCACCCGACGCCCCGCCCCCCCCCCCCCGCAG 22115

Qy      643 CCAGAGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCC 702
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      22116 CCGACGCCCCCCCCCGCGCCCCCGCCCCGACCCCCGACCCCCCGCGCCCCGCCC 22175

Qy      703 CTGGCGGAGCCCGCGCGCCCCCTTCCACGCCGCGCGCCCAAGCGC 750
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Db      22176 CCGCCCCCCCCCGGCCCCCCCCCGCGGCGCGGCGCCCCACCCC 22223

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RESULT 13

US-09-894-998A-35/c

; Sequence 35, Application US/09894998A

; Patent No. 6537555

; GENERAL INFORMATION:

; APPLICANT: Hosken, Nancy Ann

; APPLICANT: Craig H. Day

; APPLICANT: Davin C. Dillon

; APPLICANT: McGowan, Patrick

; APPLICANT: Sleath, Paul R.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TITLE OF INVENTION: TREATMENT OF HERPES SIMPLEX VIRUS INFECTION

; FILE REFERENCE: 210121.538

; CURRENT APPLICATION NUMBER: US/09/894,998A

; CURRENT FILING DATE: 2001-06-28

; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 35

; LENGTH: 2481

; TYPE: DNA

; ORGANISM: HSV-2

US-09-894-998A-35

Query Match 2.0%; Score 74.6; DB 4; Length 2481;

Best Local Similarity 48.7%; Pred. No. 1.7e-07;

Matches 203; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

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Qy      327 GTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGGAGGAGGACGAGGA 386
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Qy      387 GGAGGACGACGAGGACCTAGAGGAAGTGGAGGTGCTGGAGAGGAAGCCCGCAGCCGGGCT 446
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 Qy 507 GGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCGCTCCTGAGAGGCA 566
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 Db 1680 GCCCCAGTCCGAGTCCGGGGCCCGCGCGGCGCCGCCCTCTTGGCCCCACCCCCCTGGGG 1621
 Qy 627 CCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCCCGCCTCCGCCGCC 686
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 Db 1620 GGCGAGGGGCGAGCGCGGGGCGGCGGAGGAAGAGGCGGAGGACGAGGCCGCGGGGGCCCCGA 1561
 Qy 687 AGCCGGCGCGAGCCCCCTGGCGGAGCCCCGCCGCCCCCTTCCACGCCGGCCGCGCC 743
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RESULT 14

US-09-103-840A-2/c

; Sequence 2, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 4403765

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; FEATURE:

; OTHER INFORMATION: CDC 1551

; OTHER INFORMATION: "n" bases at various positions throughout the sequence

; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

Query Match 2.0%; Score 73.2; DB 3; Length 4403765;

Best Local Similarity 52.3%; Pred. No. 2.2e-05;

Matches 162; Conservative 0; Mismatches 148; Indels 0; Gaps 0;

Qy 434 CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCCGCCGCCGCCGCTGCTGGACT 493

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Qy 494 TCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCCG 553
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 Db 3926286 CCTTGCCCGCGGCGCCGACAACCCCGCCGGTTCTCCGGTGCCGGCGGCCCCGCGGCC
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Qy 554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCGC 613
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 Db 3926226 CGCCGGCGCCGGCGTTACCGCCAGTCCCACCCGCGCCGCGCTCGGCGCCAATCCCGCTGG
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Qy 614 CCGCTGCCGCGAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673
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Qy 674 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 733
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Qy 734 CGGCCGCGCC 743
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RESULT 15

US-09-103-840A-1/c

; Sequence 1, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; TITLE OF INVENTION: TUBERCULOSIS

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 4411529

; TYPE: DNA

; ORGANISM: Mycobacterium tuberculosis

; OTHER INFORMATION: H37Rv

US-09-103-840A-1

Query Match 2.0%; Score 73.2; DB 3; Length 4411529;
 Best Local Similarity 52.3%; Pred. No. 2.2e-05;
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 Qy 554 CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCG 613
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 Db 3932438 CGCCGGCGCCGGCGTTACCGCCAGTCCCACCCGCGCCGCGGTCCGGCGCCAATCCCGCTGG
 3932379

 Qy 614 CCGCTGCCGAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC 673
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 Qy 674 CGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC 733
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 Db 3932318 CACCACCGGAGCCGTTGATGCCGCCGGCAATGGCGTTGCCGCCCTGGCCGCCGACGCCGC
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 Qy 734 CGGCCGCGCC 743
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 Db 3932258 CGGCCCCGCC 3932249

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 Job time : 242.145 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 11, 2004, 01:22:50 ; Search time 1590.94 Seconds
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Perfect score: 3741
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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
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- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

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1	3739.4	100.0	4684	9	US-09-893-348-17	Sequence 17, Appl
2	3065.4	81.9	3492	12	US-10-267-502-214	Sequence 214, App
3	2343.6	62.6	4053	9	US-09-758-140-5	Sequence 5, Appli
4	2343.6	62.6	4053	9	US-09-972-599A-5	Sequence 5, Appli
5	2343.6	62.6	4053	17	US-10-717-597-310	Sequence 310, App
6	2343.6	62.6	4632	15	US-10-060-036-53	Sequence 53, Appl
7	2289.2	61.2	3579	9	US-09-789-386-1	Sequence 1, Appli
8	2289.2	61.2	3579	9	US-09-893-348-22	Sequence 22, Appl
9	2289.2	61.2	3579	12	US-10-267-502-212	Sequence 212, App
10	2289.2	61.2	3579	17	US-10-327-213-8	Sequence 8, Appli
11	2289.2	61.2	3579	17	US-10-466-258-8	Sequence 8, Appli
12	1088.8	29.1	1980	16	US-10-220-891-22	Sequence 22, Appl
13	809.8	21.6	2782	15	US-10-205-194-165	Sequence 165, App
14	497.4	13.3	799	13	US-10-660-946-2	Sequence 2, Appli
15	497.4	13.3	1122	9	US-09-789-386-5	Sequence 5, Appli
16	497.4	13.3	1160	15	US-10-175-523-156	Sequence 156, App
17	497.4	13.3	1785	16	US-10-439-388-62	Sequence 62, Appl
18	497.4	13.3	2052	17	US-10-466-258-3	Sequence 3, Appli
19	497.4	13.3	2235	15	US-10-060-036-54	Sequence 54, Appl
20	495.8	13.3	994	12	US-09-978-360A-110	Sequence 110, App
21	495.8	13.3	1610	9	US-09-765-205-5	Sequence 5, Appli
22	484.8	13.0	2610	17	US-10-641-643-382	Sequence 382, App
23	483.6	12.9	868	9	US-09-789-386-3	Sequence 3, Appli
24	475	12.7	1798	17	US-10-466-258-10	Sequence 10, Appl
25	468	12.5	1514	13	US-09-823-245A-349	Sequence 349, App
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27	374	10.0	422	9	US-09-960-352-11567	Sequence 11567, A
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29	302.6	8.1	423	9	US-09-960-352-9092	Sequence 9092, Ap
30	266.4	7.1	668	16	US-10-264-237-163	Sequence 163, App
31	259	6.9	566	13	US-10-085-783A-17576	Sequence 17576, A
32	259	6.9	566	16	US-10-242-535A-17576	Sequence 17576, A
33	254	6.8	1520	15	US-10-084-817-333	Sequence 333, App
34	253.2	6.8	2331	12	US-10-267-502-213	Sequence 213, App
35	253.2	6.8	3202	9	US-09-954-456-210	Sequence 210, App
36	253.2	6.8	3202	13	US-10-342-887-386	Sequence 386, App
37	253.2	6.8	3202	13	US-10-172-118-386	Sequence 386, App
38	249.2	6.7	431	9	US-09-960-352-2205	Sequence 2205, Ap
39	247.2	6.6	2343	12	US-10-267-502-215	Sequence 215, App
40	244.4	6.5	1502	15	US-10-205-219-94	Sequence 94, Appl
41	242.4	6.5	1473	15	US-10-205-194-128	Sequence 128, App
42	231.8	6.2	3637	16	US-10-108-260A-449	Sequence 449, App
43	231.8	6.2	3637	16	US-10-159-563-443	Sequence 443, App
44	228.8	6.1	711	13	US-10-408-967-1	Sequence 1, Appli
45	228.8	6.1	1330	15	US-10-106-698-1945	Sequence 1945, Ap

ALIGNMENTS

RESULT 1

US-09-893-348-17

; Sequence 17, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:


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; APPLICANT: EISENBACH-SCHWARTZ, Michal
; APPLICANT: COHEN, Irun R.
; APPLICANT: BESERMAN, Pierre
; APPLICANT: MOSONEGO, Alon
; APPLICANT: MOALEM, Gila
; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND
THEIR USES
; FILE REFERENCE: EIS-SCHWARTZ=2A
; CURRENT APPLICATION NUMBER: US/09/893,348
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/314,161
; PRIOR FILING DATE: 1999-05-19
; PRIOR APPLICATION NUMBER: US 09/218,277
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: PCT/US98/14715
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 4684
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (253)..(3744)
; OTHER INFORMATION:
US-09-893-348-17

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Query Match          100.0%; Score 3739.4; DB 9; Length 4684;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3740; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy     61 ATCGCGAAGGCAGCAGAAAGCAGTCTCATTGTTCGGGGAGCCGTCGCCTCTGCAGGTTCTT 120
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Qy    121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA 180
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Db    121 CGGCTCGGCTCGGCACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACA 180

Qy    181 ACCGCCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240
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Db    181 ACCGCCCCGCGACTCTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGC 240

Qy    241 GACCCGCCAGCCATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGC 300
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Qy    301 CCGCCCCGGCCTCCGCCCCGCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAG 360
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Db	481	CCGCTGCTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCC	540
Qy	541	GCGCCCCCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCG	600
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Qy	601	CCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCT	660
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Qy	1081	TTAGCAGAATTTTCAGAATTAGAATATTAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Db	1081	TTAGCAGAATTTTCAGAATTAGAATATTAGAAATGGGATCATCTTTTAAAGGCTCCCCA	1140
Qy	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200
Db	1141	AAAGGAGAGTCAGCCATATTAGTAGAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAA	1200

Qy	1201	GACAAAGAGGATTTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCTGTGGGT	1260
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Qy	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Db	1321	TCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGG	1380
Qy	1381	GAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTGGAA	1440
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Qy	1441	AGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAGGAT	1500
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Qy	1501	AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC	1560
Db	1501	AGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAGAACCTGTGAAGGACAGC	1560
Qy	1561	TCCAGAGCATATATTACCTGTGCTTCTTTACCTCAGCAACCGAAAGCACCACAGCAAAC	1620
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Qy	1801	GAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCATGT	1860
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Qy	2101	GAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAAGCTTGAGCCTGAAAACCCCCACCA	2160
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Qy	2221	CCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Db	2221	CCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCGTGT	2280
Qy	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Db	2281	GATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTATTCA	2340
Qy	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Db	2341	GAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCTCTCA	2400
Qy	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCCTGAAGTCCCACAAACA	2460
Db	2401	CCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCCTGAAGTCCCACAAACA	2460
Qy	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Db	2461	CAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTAGCC	2520
Qy	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAAGCCATATTTAGAG	2580
Db	2521	CAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAAGCCATATTTAGAG	2580
Qy	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Db	2581	TCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCAACATTG	2640
Qy	2641	ACCAAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Db	2641	ACCAAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTATTCAAAT	2700
Qy	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Db	2701	GATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCAGATTCA	2760
Qy	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAGTGCTAAAGATGATTCTCCT	2820
Db	2761	TCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTCAGTGCTAAAGATGATTCTCCT	2820
Qy	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Db	2821	AAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCTAATATC	2880
Qy	2881	CAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940

Db	2881	CAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTCAAGAAT	2940
Qy	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Db	2941	ATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCCAGTGTA	3000
Qy	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Db	3001	TCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAAATGGGC	3060
Qy	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Db	3061	AGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAACTTCCTTCTGACACA	3120
Qy	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAACTTCAGTT	3180
Db	3121	GAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAACTTCAGTT	3180
Qy	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Db	3181	GTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGCTTA	3240
Qy	3241	TTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAACGGCCTACATTGCCTTG	3300
Db	3241	TTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAACGGCCTACATTGCCTTG	3300
Qy	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Db	3301	GCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATCCAG	3360
Qy	3361	AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Db	3361	AAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCAGAG	3420
Qy	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAA	3480
Db	3421	GAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACATAAAAGAA	3480
Qy	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Db	3481	CTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTGATG	3540
Qy	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG	3600
Db	3541	TGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCTCTG	3600
Qy	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Db	3601	ATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCATTAT	3660
Qy	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Db	3661	CTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATCCCT	3720
Qy	3721	GGATTGAAGCGCAAAGCAGAT	3741
Db	3721	GGATTGAAGCGCAAAGCAGAT	3741

RESULT 2

US-10-267-502-214

; Sequence 214, Application US/10267502
 ; Publication No. US20040071700A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kim, Jaeseob
 ; APPLICANT: Galant, Ron
 ; TITLE OF INVENTION: Obesity Linked Genes
 ; FILE REFERENCE: LSD-07416
 ; CURRENT APPLICATION NUMBER: US/10/267,502
 ; CURRENT FILING DATE: 2003-01-27
 ; NUMBER OF SEQ ID NOS: 439
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 214
 ; LENGTH: 3492
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-267-502-214

Query Match 81.9%; Score 3065.4; DB 12; Length 3492;
 Best Local Similarity 93.6%; Pred. No. 0;
 Matches 3286; Conservative 0; Mismatches 181; Indels 42; Gaps 7;

Qy	253	ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT	312
Db	1	ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCGCGGATAGCCCGCCCCGGCCC	60
Qy	313	CCGCCCCGCCTTCAAGTACCAGTTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG	372
Db	61	CCGCCCCGCCTTCAAGTACCAGTTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAAGAC	120
Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG	432
Db	121	GAGGAG---GAGGAGGAGGACGACGAGGACCTGGAGGAATTGGAGGTGCTGGAGAGGAAG	177
Qy	433	CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCGCCGCCGCTGCTGGAC	492
Db	178	CCCGCAGCCGGGCTGTCCGCAGTTCCGGT---GCCCCCGCCGCCGCCGCCGCTGCTGGAC	234
Qy	493	TTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCTGCC	552
Db	235	TTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCCCACC	294
Qy	553	GCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCCTGCCG	612
Db	295	GCCCCCTGAGAGGCAGCCGTCTTGGGAACGCAGCCCCGCGGCGTCCGCGCCATCCCTGCCG	354
Qy	613	CCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCC	672
Db	355	CCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCGGAGGACGACGAGCCTCCAGCG-----	408
Qy	673	CCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACG	732
Db	409	CGGCCTCCGGCGCCAGCCGGCGCGAGCCCCCTAGCGGAGCCCGCCGCGCCCCCTTCCACG	468

Qy	733	CCGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTGTCTTCCT	792
Db	469	CCGGCCGCGCCCAAGCGCAGGGGCTCGGGCTCAGTGGATGAGACCCTTTTGTCTTCCT	528
Qy	793	GCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTGATGGAGCAG	852
Db	529	GCTGCATCTGAGCCTGTGATACCCTCCTCTGCAGAAAAAATTATGGATTGAAGGAGCAG	588
Qy	853	CCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCT	912
Db	589	CCAGGTAACACTGTTTCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGTTTGAAACTGCT	648
Qy	913	GCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTT	972
Db	649	GCCTCTCTTCCTTCTCTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACACGGATACCTT	708
Qy	973	GGTAACTTATCAGCAGTGTCTCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCT	1032
Db	709	GGTAACTTATCAGCAGTGGCATCCACAGAAGGAACATTGAAGAACTTTAAATGAAGCT	768
Qy	1033	TCTAAAGAGTTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTT	1092
Db	769	TCTAGAGAATTGCCAGAGAGGGCAACAAATCCATTTGTAAATAGAGAGTCAGCAGAGTTT	828
Qy	1093	TCAGAATTAGAATATTCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCA	1152
Db	829	TCAGTATTAGAATACTCAGAAATGGGATCATCTTTCAATGGCTCCCCAAAAGGAGAGTCA	888
Qy	1153	GCCATATTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGAGGAT	1212
Db	889	GCCATGTTAGTAGAAAAACACTAAGGAAGAAGTAATTGTGAGGAGTAAAGACAAAGAGGAT	948
Qy	1213	TTAGTTTGTAGTGCAGCCCTTCACAGTCCACAAGAATCACCT-----GTG	1257
Db	949	TTAGTTTGTAGTGCAGCCCTTCATAATCCACAAGAGTCACCTGCGACCCTTACTAAAGTG	1008
Qy	1258	GGTAAAGAAGACAGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAG	1317
Db	1009	GTTAAAGAAGACGGAGTTATGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGAAA	1068
Qy	1318	ATGTCAGTAGTAGCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCA	1377
Db	1069	ATGTCAGTGGTAGCACCTGTGAGGGAAGAGTATGCAGATTTAAGCCATTTGAACAAGCA	1128
Qy	1378	TGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATGTG	1437
Db	1129	TGGGAAGTGAAAGATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCTAATATG	1188
Qy	1438	GAAAGTAAAGTGGACAGAAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG	1497
Db	1189	GAAAGTAAAGTGGACAAAAAATGCTTTGAAGATAGCCTGGAGCAAAAAAGTCATGGGAAG	1248
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1249	GATAGTGAAGGCAGAAATGAGAATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1308
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCTCAGCAACCGAAAGCACCACAGCA	1617

Db	1309	GGCTCCAGAGCGTACATCACCTGTGATTCCCTTTACCTCAGCAACCGAGAGTACTGCAGCA	1368
Qy	1618	AACACTTTCCCTTTGTGTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAATA	1677
Db	1369	AACATTTTCCCTGTGCTAGAAGATCACACTTCAGAAAATAAAACAGATGAAAAAAAAATA	1428
Qy	1678	GAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTC	1737
Db	1429	GAAGAAAGGAAGGCCCAAATTATAACAGAGAAGACTAGCCCCAAAACGTCAAATCCTTTC	1488
Qy	1738	CTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCAAAGGTG	1797
Db	1489	CTTGTAGCAATACATGATTCCGAGGCAGATTATGTCACAACAGATAATTTATCAAAGGTG	1548
Qy	1798	ACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAGGAAGCA	1857
Db	1549	ACTGAGGCAGTAGTGGCAACCATGCCTGAAGGTCTAACGCCAGATTTAGTTCAGGAAGCA	1608
Qy	1858	TGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGAC	1917
Db	1609	TGTGAAAGTGAAGTGAACGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAAGTGGAC	1668
Qy	1918	TTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTTTGCCCCA	1977
Db	1669	TTGGTCCAGACATCAGAAGCTATACAAGAGTCAATTTACCCACAGCACAGCTTTGCCCCA	1728
Qy	1978	TCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTTGCTGATATTGTTATGGAAGCA	2037
Db	1729	TCATTTGAGGAAGCTGAAGCAACTCCGTCAACAGTTTTTGCTGATATTGTTATGGAAGCT	1788
Qy	2038	CCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTATCCCCA	2097
Db	1789	CCATTAAATTCTCTCCTTCCAAGCACTGGTGCTTCTGTAGCGCAGCCCAGTGCATCCCCA	1848
Qy	2098	CTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAACCCCCCA	2157
Db	1849	CTAGAAGTACCGTCTCCAGTTAGTTATGACGGTATAAAGCTTGAGCCTGAAAATCCCCCA	1908
Qy	2158	CCATATGAAGAAGCCATGAATGTAGCACTAAAAGCTTTGGGAACAAAGGAAGGAATAAAA	2217
Db	1909	CCATATGAAGAAGCCATGAGTGTAGCACTAAAAACATCGGACGCAAAGGAAGAAATTAAA	1968
Qy	2218	GAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATATCCATTGCG	2277
Db	1969	GAGCCTGAAAGTTTTAATGCAGCTGCTCAGGAAGCAGAAGCTCCTTATATATCCATTGCA	2028
Qy	2278	TGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTCTCTAATTAT	2337
Db	2029	TGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGGGTTCTCTAATTAT	2088
Qy	2338	TCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTGGAGGATTCC	2397
Db	2089	TCAGAAATAGCAAAATTTGAGAAGTCGGTACCTGATCACTGTGAGCTCGTGGATGATTCC	2148
Qy	2398	TCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAAGTCCCACAA	2457

Db	2149	TCACCCGAATCTGAACCACTTACTTATTTAGTGATGATTCGATTCTCTGAAGTCCCACAA	2208
Qy	2458	ACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTA	2517
Db	2209	ACACAAGAGGAGGCTGTGATGCTAATGAAGGAGAGTCTCACTGAAGTGTCTGAGACAGTA	2268
Qy	2518	GCCCAGCACAAA---GAGGAGAGACTTAGTGCCTCACCTCAGGAGCTAGGAAAGCCATAT	2574
Db	2269	ACACAACACAAACATAAGGAGAGACTTAGTGCCTCACCTCAGGAGGTAGGAAAGCCATAT	2328
Qy	2575	TTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGCTGCATCTAATGACATTCCA	2634
Db	2329	TTAGAGTCTTTTCAGCCCAATTTACATATTACAAAAGATGCTGCATCTAATGAAATTCCA	2388
Qy	2635	ACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTAT	2694
Db	2389	ACATTGACCAAAAAGGAGACAATTTCTTTGCAAATGGAAGAGTTTAATACTGCAATTTAT	2448
Qy	2695	TCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAAACATTTTCA	2754
Db	2449	TCCAATGATGACTTACTTTCTTCTAAGGAAGACAAAATGAAAGAAAGTGAAACATTTTCC	2508
Qy	2755	GATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTAGTAAAGATGAT	2814
Db	2509	GATTCATCTCCCATTGAGATAATAGATGAGTTTCCACATTTGTGCTAGTAAAGATGAT	2568
Qy	2815	TCTCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAAAGTGAAATTGCT	2874
Db	2569	TCTCCT-----AAGGAGTACACTGACCTAGAAGTATCCAACAAAAGTGAAATTGCT	2619
Qy	2875	AATATCCAAAGCGGGGCAGATTCAATGCCTTGCTTAGAATTGCCCTGTGACCTTTCTTTC	2934
Db	2620	AATGTCCAGAGCGGGGCCAATTCGTTGCCTTGCTCAGAATTGCCCTGTGACCTTTCTTTC	2679
Qy	2935	AAGAATATATATCCTAAAGATGAAGTACATGTTTCAGATGAATTCTCCGAAAATAGGTCC	2994
Db	2680	AAGAATACATATCCTAAAGATGAAGCACATGTCTCAGATGAATTCTCCAAAAGTAGGTCC	2739
Qy	2995	AGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCTTTGGAACCTCAGACAGAA	3054
Db	2740	AGTGTATCTAAGGTGCCCTTATTGCTTCCAAATGTTTCTGCTTTGGAATCTCAAATAGAA	2799
Qy	3055	ATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCAGAGAAAAAAGTTTCCTTCT	3114
Db	2800	ATGGGCAACATAGTTAAACCCAAAGTACTTACGAAAGAAGCAGAGGAAAAAAGTTTCCTTCT	2859
Qy	3115	GACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTATTGTCAGCAGAGCTGAGTAAAGT	3174
Db	2860	GATACAGAGAAAGAGGACAGATCCCTGACAGCTGTATTGTCAGCAGAGCTGAATAAAAGT	2919
Qy	3175	TCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTG---TTTGGT	3231
Db	2920	TCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTATTTTGGT	2979
Qy	3232	GCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTACGATTGTCAGTGTAAACGGCTTAC	3291
Db	2980	GCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTACGATTGTCAGTGTAAACGGCTTAC	3039

Qy 3292 ATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAG 3351
 |||
 Db 3040 ATTGCCTTGGCCCTGCTCTCTGTGACTATCAGCTTTAGGATATATAAGGGTGTGATCCAA 3099
 Qy 3352 GCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTAGAATCTGAAGTTGCT 3411
 |||
 Db 3100 GCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCATATTTGGAATCTGAAGTTGCC 3159
 Qy 3412 ATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACA 3471
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 Db 3160 ATATCAGAGGAATTGGTTCAGAAATATAGTAATTCTGCTCTTGGTCATGTGAACAGCACA 3219
 Qy 3472 ATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTAGTTGATTCCCTGAAGTTTGCA 3531
 |||
 Db 3220 ATAAAAGAAATTGAGGCGTCTCTTCTTAGTTGATGATTAGTTGATTCCCTGAAGTTTGCA 3279
 Qy 3532 GTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCATGGTCTGACACTACTGATT 3591
 |||
 Db 3280 GTGTTGATGTGGGTATTTACTTACGTTGGTGCCTTGTTCATGGTTTGACACTACTGATT 3339
 Qy 3592 TTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGGCATCAGGTGCAGATA 3651
 |||
 Db 3340 TTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATATATGAACGGCATCAGGCGCAGATA 3399
 Qy 3652 GATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCA 3711
 |||
 Db 3400 GATCATTATCTAGGACTTGCAAACAAGAGCGTTAAGGATGCCATGGCCAAAATCCAAGCA 3459
 Qy 3712 AAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
 |||
 Db 3460 AAAATCCCTGGATTGAAGCGCAAAGCAGA 3488

RESULT 3

US-09-758-140-5

; Sequence 5, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.

; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of Axonal Growth

; FILE REFERENCE: 44574-5073-US

; CURRENT APPLICATION NUMBER: US/09/758,140

; CURRENT FILING DATE: 2001-01-12

; PRIOR APPLICATION NUMBER: US 60/175,707

; PRIOR FILING DATE: 2000-01-12

; PRIOR APPLICATION NUMBER: US 60/207,366

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 60/236,378

; PRIOR FILING DATE: 2000-09-29

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 4053

; TYPE: DNA

; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human mRNA for No. US20020012965A1 protein (KIAA0886,
GenBank
; OTHER INFORMATION: Accession No. US20020012965A1 AB020693)
US-09-758-140-5
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Query Match          62.6%;  Score 2343.6;  DB 9;  Length 4053;
Best Local Similarity 81.3%;  Pred. No. 0;
Matches 3017;  Conservative 0;  Mismatches 574;  Indels 119;  Gaps 21;
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Qy      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
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Db      16 CTCGGCTCAGTCGGCCCAGCCCCCTCTCAGTCCTCCCCAACCCCCACAACCGCCCGCGGCT 75

Qy      194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      76 CTGAGACGCGGCCCCGGCGGCGGCGGCGAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 134

Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCACCCCGGCCG 191

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      249 GAGGAGGAAGAGGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 308

Qy      433 CCCGACCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCGCCGCGCCGCTG 486
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      309 CCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCCCACCGCCCCCTGCCGCCGCGCGCCCCCTG 368

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGGCCGCTGCCGCCGCGGCC 546
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      369 ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGCCGCGCTCCC 428

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      429 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTCGTACCGTGCCC 488

Qy      598 GCGCCATCCCTGCCGCCCGCTGCCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      489 GCGCCATCCCCGCTGTCTGCTGCCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 548

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      549 CCTCCGGCCCGGCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTG 608

Qy      712 -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      609 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGGCCGCGCCCAAGCGC 668

Qy      751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGTCTTCTGCTGCATCTGAGCCT 807
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Db	669	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGGCTCTTCCTGCTGCATCTGAGCCT	728
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	786	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	845
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	905
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	906	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	965
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	966	GAGAAGGCCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1025
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1026	TCAGAAATGGGATCATCGTTCAAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1085
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	1086	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1145
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1206	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGA	1265
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1266	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1325
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1326	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1382
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGAAG	1497
Db	1383	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAA	1442
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1443	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAGGTATAAAGGAT	1502
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614

Db	1503	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAAACCAGCAGCAACTGAGAGCATTGCA	1562
Qy	1615	GCAAACACTTTTCCTTTTGTAGAAAGATCATACTTCAGAAAAATAAAACAGATGAAAAAAA	1674
Db	1563	ACAAACATTTTTCCTTTTGTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAAAA	1622
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1623	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1682
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1683	CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1742
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1743	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1802
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1803	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1862
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1863	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1922
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1923	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1982
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2042
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2099
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2100	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2159
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2160	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2219
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	2220	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTCTGCTGAACCAGCTCCGGATTTT	2279
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2280	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2339
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2340	GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2399

Qy	2449	GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2400	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2459
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTC	2799
Db	2700	ACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2759
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2760	AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2819
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGCACAGAATTG	2879
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2880	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2939
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3120	TTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270
Db	3180	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTTTTCATTGACAGTATTTCAGC	3239


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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(3710)
; OTHER INFORMATION: Human DNA encoding for No. US20020077295A1o protein
(KIAA0886, GenBank
; OTHER INFORMATION: Accession No. US20020077295A1 AB020693)
US-09-972-599A-5
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Query Match          62.6%;  Score 2343.6;  DB 9;  Length 4053;
Best Local Similarity 81.3%;  Pred. No. 0;
Matches 3017;  Conservative 0;  Mismatches 574;  Indels 119;  Gaps 21;
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Qy      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      16 CTCGGCTCAGTCGGCCCAGCCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCGCGGCT 75

Qy      194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      76 CTGAGACGCGGCCCCGGCGGCGGCGGCGAGCAGCTGCAGCATCATC-TCCACCCTCCAGCC 134

Qy      253 ATGGAAGACATAGACCAGTTCGTTCGTTCTCCTCGTCCACGGACAGCCCGCCCGGCCCT 312
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCACCCCGGCCG 191

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      249 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 308

Qy      433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCCGCGCCGCTG 486
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      309 CCCGCCGCCGGGCTGTCCGCAGGCCCCAGTGCCCCACCGCCCTGCCGCCGGCGCGCCCTG 368

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      369 ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 428

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      429 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC 488

Qy      598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      489 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 548

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      549 CCTCCGGCCCCGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 608

Qy      712 -----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      609 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGGCCGCGCCCAAGCGC 668
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Qy	751	AGGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGGCTCTTCCTGCTGCATCTGAGCCT	807
Db	669	AGGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGGCTCTTCCTGCTGCATCTGAGCCT	728
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
Qy	868	TCGTCCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	786	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	845
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAACTTGTCAACA	905
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	906	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	965
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	966	GAGAAGGCCAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1025
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1026	TCAGAAATGGGATCATCGTTAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1085
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	1086	AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1145
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1206	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1265
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAA	1389
Db	1266	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAA	1325
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1326	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1382
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTGGGAAG	1497
Db	1383	GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAA	1442
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1443	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1502

Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614
Db	1503	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1562
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAAATAAAACAGATGAAAAAAAA	1674
Db	1563	ACAAACATTTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAAATAAGACCGATGAAAAAAAA	1622
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1623	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1682
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1683	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1742
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1743	AAGGTGACTGAGGAAGTCTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1802
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1803	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1862
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1863	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1922
Qy	1972	TGCCCATCATTTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1923	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1982
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2042
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2099
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2100	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAAGTATCAGGAATAAAGGAA	2159
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2160	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2219
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTC	2328
Db	2220	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTC	2279
Qy	2329	TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2280	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2339
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448

Db	2340	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2399
Qy	2449	GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2400	GTTCCACAAAAACAAGATGAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2459
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA	2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTTA	2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
Qy	2740	AGTGAAACATTTTCAGATTCACTCCGATTGAGATAATAGATGAATTTCCCACGTTTGTC	2799
Db	2700	ACTGAAACGTTTTCAGATTCACTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2759
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2760	AGTTCTAAAACTGATTTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2819
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGACAGAATTG	2879
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2880	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2939
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3120	TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270

; SEQ ID NO 310
; LENGTH: 4053
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-310

Query Match 62.6%; Score 2343.6; DB 17; Length 4053;
Best Local Similarity 81.3%; Pred. No. 0;
Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

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Qy      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCCGCGACT 193
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Db      16  CTCGGCTCAGTCGGCCCAGCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCCGCGGCT 75

Qy      194 CTGAGGAGAAGCGGC-CCTGCGGGGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      76  CTGAGACGCGGCCCCGGCGGGCGGCAGCAGCTGCAGCATCATC-TCCACCCCTCCAGCC 134

Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
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Db      135 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCACCCCGGCCG 191

Qy      313 CCGCCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGAGGAG 372
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      192 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 248

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      249 GAGGAGGAAGAGGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 308

Qy      433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCGCCGCGCCGCTG 486
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      309 CCCGCCGCGGGCTGTCCGCGGCCCCAGTGCCCAACCGCCCTGCCGCGGGCGCGCCCTG 368

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCC 546
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      369 ATGGACTTCGGAATGACTTCGTGCCGCGGCGCCCCGGGGACCCCTGCCGCGCGCTCCC 428

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      429 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTCGACCGTGCCC 488

Qy      598 GCGCCATCCCTGCCGCCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      489 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 548

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG----- 711
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      549 CCTCCGGCCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 608

Qy      712 -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      609 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGGCCGCGCCCAAGCGC 668

Qy      751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      669 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 728
```

Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTGATGGAGCAGCCAGGTAACACTGTT	867
Db	729	GTGATACGCTCCTCTGCAGAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	785
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCCTCTCTTCCTTCT	927
Db	786	TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAACTGCTGCCTCTCTTCCTTCT	845
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA	987
Db	846	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAAATTTGTCAACA	905
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	906	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	965
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	966	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC	1025
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	1026	TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	1085
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	1086	AATCCTAGGAAGAAATAATCCTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1145
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1146	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1205
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1206	GAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1265
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1266	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1325
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1326	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1382
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG	1497
Db	1383	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACCTAATCACGAAAAA	1442
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1443	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1502
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA	1614
Db	1503	CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1562

Qy	1615	GCAAAACACTTTCCCTTTGTTAGTAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1563	ACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1622
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1623	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1682
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1683	CCTTTCCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1742
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1743	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1802
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAAGATTGCTTATGAAACAAAA	1911
Db	1803	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1862
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1863	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1922
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1923	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTACCAGTTTTGCCTGACATTGTTATG	1982
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1983	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA	2042
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAC	2151
Db	2043	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAACATGAGCCTGAAAC	2099
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2100	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2159
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTAAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2160	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2219
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	2220	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTT	2279
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCGAACACGCTGAGCTAGTG	2388
Db	2280	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATCTGAGCTAGTT	2339
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTCGATTCCTGAA	2448
Db	2340	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2399
Qy	2449	GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502

Db	2400	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2459
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2460	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2519
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2520	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2579
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2580	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2639
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAGAA	2739
Db	2640	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2699
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2700	ACTGAAACGTTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2759
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2760	AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2819
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916
Db	2820	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTTCATTGCCTTGCACAGAATTG	2879
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2880	CCCCATGACCTTTCTTTGAAGAACATAACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2939
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2940	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2999
Qy	3031	TCTGCTTTTGGAACTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3000	TCTGCTTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3059
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA	3150
Db	3060	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3119
Qy	3151	TTGTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3120	TTTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3179
Qy	3211	AAGACTGGAGTGGTGTTTGGTGCCAGCTTATTCTGCTGCTGTCTCTGACAGTGTTTCAGC	3270
Db	3180	AAGACTGGAGTGGTGTTTGGTGCCAGCCTATTCTGCTGCTTTTCATTGACAGTATTTCAGC	3239
Qy	3271	ATTGTTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330


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Db      3240 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3299
Qy      3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3300 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3359
Qy      3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
      ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3360 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3419
Qy      3451 CTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3420 CTTGGTCATGTGAACAGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3479
Qy      3511 GTTGATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3480 GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTACCTATGTTGGTGCCTTGTTT 3539
Qy      3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3540 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACCTCTTCAGTGTTCCTGTTATTTAT 3599
Qy      3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3600 GAACGGCATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3659
Qy      3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      3660 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3709

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RESULT 6

US-10-060-036-53

; Sequence 53, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER

; FILE REFERENCE: 210121.566

; CURRENT APPLICATION NUMBER: US/10/060,036

; CURRENT FILING DATE: 2002-01-30

; NUMBER OF SEQ ID NOS: 4560

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 53

; LENGTH: 4632

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-060-036-53

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Query Match          62.6%;  Score 2343.6;  DB 15;  Length 4632;
Best Local Similarity 81.3%;  Pred. No. 0;

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Matches 3017; Conservative 0; Mismatches 574; Indels 119; Gaps 21;

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Qy      134 CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCAACCCCCACAACCGCCCGCGACT 193
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      23  CTCGGCTCAGTCGGCCAGCCCCCTCTCAGTCCTCCCAACCCCCACAACCGCCCGCGGCT 82

Qy      194 CTGAGGAGAAGCGGC-CCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCC 252
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      83  CTGAGACGCGGCCCCGGCGGCGGCGGCAGCAGCTGCAGCATCATC-TCCACCTCCAGCC 141

Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCT 312
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      142 ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCCAACCCGGCCG 198

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      199 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 255

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      256 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 315

Qy      433 CCCGCAGCCGGGCTGTCCGCAGTGCGGTGC-----CGCCCGCCGCCGCCGCCCGCTG 486
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      316 CCCGCCGCCGGGCTGTCCGCAGTGCAGTGCACCGCCCTGCCGCCGCCGCCCGCTG 375

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGGCCGCTGCCGGCCGCCGCC 546
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      376 ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 435

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      436 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTGCTCGACCGTGCCC 495

Qy      598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      496 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 555

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG----- 711
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      556 CCTCCGGCCCGGCCTCCCCCTCCTCCCCCGGCCAGCGTGAGCCCCAGGCAGAGCCCGTG 615

Qy      712 -----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      616 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGGCCGCGCCCAAGCGC 675

Qy      751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      676 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 735

Qy      808 GTGATACCCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      736 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 792

Qy      868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT 927
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      793 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCTTCTCTTCCTTCT 852
```

Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987
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Db 853 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 912

Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
 || | | | | ||||| || ||||| | | | ||||| ||||| || ||

Db 913 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 972

Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107
 |||| |||| || || | | || ||||| |||| ||||| ||||| |||||

Db 973 GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 1032

Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167
 ||||| ||||| |||| || | | || ||||| |||| || || || || || || || ||

Db 1033 TCAGAAATGGGATCATCGTTCAAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 1092

Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
 || || || ||||| |||| || || || || || || || || || || || || ||

Db 1093 AATCCTAGGGAAGAAATAATCGTGAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1152

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269
 ||||| | || ||||| | |||| ||||| ||||| ||

Db 1153 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1212

Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329
 ||||| ||||| ||||| || || || ||||| ||||| | | |||| | |

Db 1213 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGA 1272

Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389
 || || || ||||| || ||||| ||||| || ||||| || || ||||| |||||

Db 1273 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1332

Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437
 |||| | || | || || || || ||||| |||| | || || || || ||

Db 1333 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1389

Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497
 ||||| ||||| || ||||| || | ||||| ||||| || || | ||

Db 1390 GAAAGTAAAGTGGATAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA 1449

Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557
 ||||| || || ||||| || ||||| ||||| ||||| || || ||||

Db 1450 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1509

Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTA---CCTCAGCAACCGAAAGCACCACA 1614
 | || ||||| || ||||| ||||| | ||||| || |||| ||

Db 1510 CGTTCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1569

Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA 1674
 ||||| || ||||| |||| ||||| ||||| || ||||| |||||

Db 1570 ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA 1629

Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1630 ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC 1689

Qy	1732	CCTTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1690		
		CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1749
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1750		
		AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCTGACTCCAGATTTAGTACAG	1809
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAA	1911
Db	1810		
		GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAA	1869
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1870		
		ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1929
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1930		
		TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1989
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1990		
		GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	2049
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	2050		
		TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	2106
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	2107		
		CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2166
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2167		
		GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2226
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	2227		
		TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTT	2286
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2287		
		TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2346
Qy	2389	GAGGATTCCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCCTGAA	2448
Db	2347		
		GAAGATTCCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2406
Qy	2449	GTCCCAACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2407		
		GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2466
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2467		
		TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2526
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619

Db	2527	 GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2586
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2587	 CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2646
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2647	 AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2706
Qy	2740	AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2707	 ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2766
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2767	 AGTTCATAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2826
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2827	 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGCCACAGAATTG	2886
Qy	2917	CCCTGTGACCTTTCTTTCAAGAAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2887	 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2946
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2947	 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	3006
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	3007	 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	3066
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAAGAGGACAGATCCCTGTGCTGTA	3150
Db	3067	 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	3126
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	3127	 TTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3186
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTGAGC	3270
Db	3187	 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC	3246
Qy	3271	ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3247	 ATTGTCAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3306
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3390
Db	3307	 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA	3366
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTTCAGAAATACAGTAATTCTGCT	3450

Db	58	CAGCCCGCGTTCAAGTACCAGTTTCGTGAGGGAGCCCCGAGGACGAGGAG---GAAGAAGAG	114
Qy	373	GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAAGTGGAGGTGCTGGAGAGGAAG	432
Db	115	GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG	174
Qy	433	CCCGCAGCCGGGCTGTCCGCGAGCTGCGGTGC-----CGCCCGCCGCCGCCGCGCCGCTG	486
Db	175	CCCGCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCCCTGCCGCCGCGCGCCCCCTG	234
Qy	487	CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC	546
Db	235	ATGGACTTCGGAATGACTTCGTGCCGCCGCGCCCCGCGGACCCCTGCCGGCCGCTCCC	294
Qy	547	CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC	597
Db	295	CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCTGTCGACCGTGCCC	354
Qy	598	GCGCCATCCCTGCCGCCGCTGCCGCGAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG	657
Db	355	GCGCCATCCCCGCTGTCTGCTGCCGCGAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG	414
Qy	658	CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAG-----	711
Db	415	CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG	474
Qy	712	-----CCCCGCCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC	750
Db	475	TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCCGCGCCCAAGCGC	534
Qy	751	AGGGGCTCC---GGCTCAGTGGATGAGACCCCTTTTGCTCTTCCTGCTGCATCTGAGCCT	807
Db	535	AGGGGCTCCTCGGGCTCAGTGGATGAGACCCCTTTTGCTCTTCCTGCTGCATCTGAGCCT	594
Qy	808	GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT	867
Db	595	GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT	651
Qy	868	TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT	927
Db	652	TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCTTCTCTTCCTTCT	711
Qy	928	CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTATCAGCA	987
Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167

Db 892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951
 Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
 || ||| ||||| |||| ||| | |||| || ||||| | ||||| ||| |
 Db 952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011
 Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269
 ||||| | || ||||| | |||| ||| ||||| ||
 Db 1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071
 Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329
 ||||| ||||| ||| |||| ||||| ||||| | | |||| | |
 Db 1072 GAAGTTGTGTCTTCAGAAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGA 1131
 Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389
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 Db 1132 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1191
 Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437
 |||| | ||| || |||| || ||||| |||| | ||||| || ||
 Db 1192 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1248
 Qy 1438 GAAAGTAAAGTGACAGAAAAATGCTTGGGAAGATAGCCTGGAGCAAAAAAGTCTTGGGAAG 1497
 ||||| ||||| || ||||| ||||| ||||| || || | ||
 Db 1249 GAAAGTAAAGTGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA 1308
 Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557
 ||||| || || |||| || ||||| ||||| ||||| || |||||
 Db 1309 GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1368
 Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA 1614
 | | ||||| || ||||| ||||| | ||||| || |||| | |
 Db 1369 CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA 1428
 Qy 1615 GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA 1674
 ||||| || ||||| ||||| ||||| ||||| || ||||| |||||
 Db 1429 ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA 1488
 Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1489 ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC 1548
 Qy 1732 CCTTTTCCTTGTTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791
 |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1549 CCTTTTCCTTGTTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1608
 Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 Db 1609 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1668
 Qy 1852 GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1669 GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1728
 Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1729 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1788

Qy	1972	TGCCCCATCATTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCCATCATTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAAGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTCTGCTGAACCAGCTCCGGATTC	2145
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2206	GAAGATTCCTCACCTGATTCTGAACCAAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTTA	2445
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC	2625

Qy 2800 AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC 2856
 ||| ||||| ||||| | ||||| ||||| ||| || ||||| ||||| |||||
 Db 2626 AGTTCTAAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2685

Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTGCTGCCTTGCTTAGAATTG 2916
 ||||| ||||| ||||| || || || || ||||| ||||| |||||
 Db 2686 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTGCACAGAATTG 2745

Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970
 ||| ||||| ||||| ||||| ||| || || ||||| ||||| | || ||||
 Db 2746 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2805

Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030
 ||||| || || || ||||| |||| | || |||| | || |||| || ||||
 Db 2806 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 2865

Qy 3031 TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
 ||||| ||||| |||| ||| || ||||| ||||| |||| |||| ||||
 Db 2866 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 2925

Qy 3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA 3150
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 Db 2926 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 2985

Qy 3151 TTGTGAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 2986 TTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3045

Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC 3270
 ||||| ||||| ||||| ||||| ||||| ||||| || ||||| ||||| |||||
 Db 3046 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTTCAGC 3105

Qy 3271 ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
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 Db 3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165

Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3390
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTCAGGGCA 3225

Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
 ||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3285

Qy 3451 CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
 ||||| ||||| ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 Db 3286 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3345

Qy 3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3346 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405

Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTTATTTAT 3465

Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690

Db 115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174
 Qy 433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCCGCCGCCGCCGCCGCTG 486
 ||||| ||||| ||||| || || ||||| ||||| ||||| ||||| |||||
 Db 175 CCCGCCGCCGGGCTGTCCGCAGGCCCCAGTGCCACCGCCCCCTGCCGCCGGCGCGCCCCCTG 234
 Qy 487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCCC 546
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 Db 235 ATGGACTTCGAAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294
 Qy 547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
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 Db 295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTGACCGTGCCC 354
 Qy 598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
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 Db 355 GCGCCATCCCCGCTGTCTGCTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 414
 Qy 658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG----- 711
 ||||| ||||| ||||| || || || ||||| || ||||| || || ||||| || || |||||
 Db 415 CCTCCGGCCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 474
 Qy 712 -----CCCCGCCGCCGCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCCGCCGCGCCCAAGCGC 534
 Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCCTTTTGTCTCTCCTGCTGCATCTGAGCCT 807
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 535 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCCTTTTGTCTCTCCTGCTGCATCTGAGCCT 594
 Qy 808 GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 595 GTGATACGCTCCTCTGCAGAAAA--TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 651
 Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTTGCTTGAAACTGCTGCCTCTCTTCCTTCT 927
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 652 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTTGCTTGAAACTGCTGCTTCTCTTCCTTCT 711
 Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTATCAGCA 987
 || ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771
 Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
 || || || || ||||| || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831
 Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107
 ||||| ||||| || || || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 832 GAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 891
 Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167
 ||||| ||||| ||||| || || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 892 TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951
 Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
 || ||||| ||||| ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269
 ||||| | || ||||| | ||| ||| ||||| ||
 Db 1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071
 Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329
 ||||| ||||| ||| ||| ||||| ||| | ||| |
 Db 1072 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA 1131
 Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389
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 Db 1132 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1191
 Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437
 |||| | ||| | ||| ||| || ||||| ||| | || ||
 Db 1192 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1248
 Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497
 ||||| ||||| | ||||| || ||||| ||||| ||| | ||
 Db 1249 GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAATAATCACGAAAAA 1308
 Qy 1498 GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC 1557
 ||||| | || ||||| ||| ||||| ||||| ||||| | |||||
 Db 1309 GATAGTGAAGGATAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT 1368
 Qy 1558 AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA 1614
 | | ||||| || ||||| ||||| | ||||| || ||||| ||
 Db 1369 CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA 1428
 Qy 1615 GCAAACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAAA 1674
 ||||| ||| ||||| ||||| ||||| ||||| || ||||| |||||
 Db 1429 ACAAACATTTTCCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAAA 1488
 Qy 1675 ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT 1731
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1489 ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAAACATCAAAC 1548
 Qy 1732 CCTTTCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA 1791
 |||| ||||| ||||| ||||| ||||| ||||| ||||| ||| ||
 Db 1549 CCTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA 1608
 Qy 1792 AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG 1851
 ||||| ||||| || ||| ||||| ||||| ||||| ||||| |||||
 Db 1609 AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG 1668
 Qy 1852 GAAGCATGTGAAAGTGAACTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA 1911
 ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 Db 1669 GAAGCATGTGAAAGTGAAATGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA 1728
 Qy 1912 GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT 1971
 ||||| ||||| ||||| ||||| ||| ||||| ||||| || || ||||| |||||
 Db 1729 ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT 1788
 Qy 1972 TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG 2031
 ||||| ||||| || | ||||| ||||| ||||| ||||| ||||| |||||
 Db 1789 TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG 1848

Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGT	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2206	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTA	2445
Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTCAGATTTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626	AGTTCTAAAACCTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAGCGGGGCAGATTTCATTGCCTTGCTTAGAATTG	2916

Db	2686		CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACAGAATTG	2745
Qy	2917		CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746		CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971		GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806		GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031		TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866		TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091		GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	2926		GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151		TTGTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	2986		TTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3045
Qy	3211		AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC	3270
Db	3046		AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC	3105
Qy	3271		ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3106		ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3165
Qy	3331		ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCA	3390
Db	3166		ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTACAGGGCA	3225
Qy	3391		TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT	3450
Db	3226		TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT	3285
Qy	3451		CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510
Db	3286		CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGCCTCTTCTTAGTTGATGATTTA	3345
Qy	3511		GTTGATTCCCTGAAGTTTGCAGTGTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT	3570
Db	3346		GTTGATTCTCTGAAGTTTGCAGTGTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT	3405
Qy	3571		AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT	3630
Db	3406		AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTAT	3465
Qy	3631		GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT	3690
Db	3466		GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT	3525
Qy	3691		GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA	3740

Db 3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575

RESULT 9

US-10-267-502-212
; Sequence 212, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 212
; LENGTH: 3579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-267-502-212

Query Match 61.2%; Score 2289.2; DB 12; Length 3579;
Best Local Similarity 81.5%; Pred. No. 0;
Matches 2925; Conservative 0; Mismatches 548; Indels 117; Gaps 19;

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Qy      253 ATGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCGGCCCT 312
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Db      1  ATGGAAGACCTGGACCAGTCTCCTCTGGT---CTCGTCTCGGACAGCCCAACCCGCGCCG 57

Qy      313 CCGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAG 372
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      58 CAGCCCGCGTTCAAGTACCAGTTCGTGAGGGAGCCCGAGGACGAGGAG---GAAGAAGAG 114

Qy      373 GAGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAG 432
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      115 GAGGAGGAAGAGGAGGACGAGGACGAAGACCTGGAGGAGCTGGAGGTGCTGGAGAGGAAG 174

Qy      433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCCGCCCGCGCCGCTG 486
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      175 CCCGCCCGCGGGCTGTCCGCGGCCCCAGTGCCCCACCGCCCTGCCGCGGCGCGCCCTG 234

Qy      487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      235 ATGGACTTCGGAATGACTTCGTGCCGCGCGGCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy      547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
          || | ||| || ||| ||||| || ||||| | ||||| | || |||||
Db      295 CCCGTCGCCCCGGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTCGTGACCGTGCCC 354

Qy      598 GCGCCATCCCTGCCGCCCCTGCCGCGAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      355 GCGCCATCCCCGCTGTCTGCTGCCGCGAGTCTGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy      658 CCTCCGGCGAGGCCCCCGCCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG----- 711
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      415 CCTCCGGCCCGGCCTCCCCCTCCTCCCCGGCCAGCGTGAGCCCCCAGGACAGCCCGTG 474
```


Qy 712 -----CCCGCCGCGCCCCCTTCCACGCCGCGCCGCGCCCAAGCGC 750
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 Db 475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTTCCACCCCGCGCGCCCAAGCGC 534

Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTGGCTCTTCCTGCTGCATCTGAGCCT 807
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 Db 535 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTGGCTCTTCCTGCTGCATCTGAGCCT 594

Qy 808 GTGATACCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
 |||||
 Db 595 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 651

Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCCTCTCTTCCTTCT 927
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 Db 652 TCGGCTGGTCAAGAGGATTTCCCATCTGTCCTGCTTGAAACTGCTGCTTCTCTTCCTTCT 711

Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACTTATCAGCA 987
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 Db 712 CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy 988 GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
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 Db 772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107
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 Db 832 GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC 891

Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167
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 Db 892 TCAGAAATGGGATCATCGTTTCAAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951

Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
 ||
 Db 952 AATCCTAGGGAAGAAATAATCGTGAAAAATAAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269
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 Db 1012 AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT 1071

Qy 1270 AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA 1329
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 Db 1072 GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTAATGAAAAGAGAGTTGCAGTGGAA 1131

Qy 1330 GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA 1389
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 Db 1132 GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA 1191

Qy 1390 GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG 1437
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 Db 1192 GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG 1248

Qy 1438 GAAAGTAAAGTGGACAGAAAATGCTTGAAGATAGCCTGGAGCAAAAAGTCTTGGGAAG 1497
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 Db 1249 GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA 1308

Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCCAGTACCCCAAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA	1674
Db	1429	ACAAACATTTTTCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA	1488
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1548
Qy	1732	CCTTTCTTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTTGAGGAAGCTGAAGCAACTCCGTACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT	2328
Db	2086	TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTT	2145
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388

Db	2146		TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389		GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTTCGATTCCTGAA	2448
Db	2206		GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449		GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266		GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503		GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326		TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563		GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386		GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCGTGTTA	2445
Qy	2620		TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446		CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680		AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAAGAA	2739
Db	2506		AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740		AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566		ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2625
Qy	2800		AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626		AGTTCTAAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857		GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCAATTGCCTTGCTTAGAATTG	2916
Db	2686		CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCAATTGCCTTGACAGAAATTG	2745
Qy	2917		CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746		CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971		GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806		GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031		TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866		TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091		GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	2926		GAAGCTGAGAAAAAACTTCCTTCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151		TTGTGAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210

Db 2986 TTTTCAGCAGAGCTGAGTAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3045
 Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGC 3270
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 Db 3046 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTCATTGACAGTATTCAGC 3105
 Qy 3271 ATTGTCAGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
 ||||| || ||||| |||||||||||||||||||||||||| ||||| |||||||||||||
 Db 3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165
 Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3390
 ||||| ||||| ||||||| |||||||||||||||||||||||||||||||||||||||||
 Db 3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTTCAGGGCA 3225
 Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
 ||| | ||||||||||||||||||| ||||| ||||||||||| |||||||||||||
 Db 3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCT 3285
 Qy 3451 CTTGGTCATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
 ||||||||||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3286 CTTGGTCATGTGAACAGCACAAATAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3345
 Qy 3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570
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 Db 3346 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405
 Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
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 Db 3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTTATTTAT 3465
 Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
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 Db 3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525
 Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
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 Db 3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575

RESULT 10

US-10-327-213-8

; Sequence 8, Application US/10327213

; Publication No. US20040121341A1

; GENERAL INFORMATION:

; APPLICANT: FILBIN, MARIE T.

; APPLICANT: DOMENICONI, MARCO

; APPLICANT: CAO, ZIXUAN

; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)

; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION

; FILE REFERENCE: CUNY/003

; CURRENT APPLICATION NUMBER: US/10/327,213

; CURRENT FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 8

; LENGTH: 3579

; TYPE: DNA

; ORGANISM: Homo sapiens
US-10-327-213-8

Db	712	CTGTCTCCTCTCTCAGCCGCTTCTTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA	771
Qy	988	GTGTCATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA	1047
Db	772	GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA	831
Qy	1048	GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT	1107
Db	832	GAGAAGGCAAAAACCTCTACTCATAGATAGAGATTTAACAGAGTTTTTCAGAATTAGAATAC	891
Qy	1108	TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA	1167
Db	892	TCAGAAATGGGATCATCGTTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA	951
Qy	1168	AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT	1224
Db	952	AATCCTAGGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT	1011
Qy	1225	GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC	1269
Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTTTAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAGCAAAAGACAGTTTTTAATGAAAAGAGAGTTGTCAGTGGA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAAGATAGCCTGGAGCAAAAAAGTCTTGGAAG	1497
Db	1249	GAAAGTAAAGTGGATAAAAAATGTTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAATGAGGATGCTTCTTTCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAA	1674
Db	1429	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAA	1488
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1548
Qy	1732	CCTTTCCTTGTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTTCTTGTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608

Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTAGTTTACAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGACAGCCCAGTGTA	2091
Db	1849	GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA	1908
Qy	2092	TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC	2151
Db	1909	TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC	1965
Qy	2152	CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA	2208
Db	1966	CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA	2025
Qy	2209	GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTTCAGGAAACAGAAGCTCCTTATATA	2268
Db	2026	GAAATTAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA	2085
Qy	2269	TCCATTGCGTGTGATTTAATTAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTTC	2328
Db	2086	TCTATTGCATGTGATTTAATTAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTTC	2145
Qy	2329	TCTAATTATTTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG	2388
Db	2146	TCTGATTATTTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT	2205
Qy	2389	GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGATTTCCTGAA	2448
Db	2206	GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC	2265
Qy	2449	GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A	2502
Db	2266	GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA	2325
Qy	2503	GTGTCTGAGACAGTAGCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA	2562
Db	2326	TTTGAGTCAATGATAGAATATGAAAATAAGGAAAACTCAGTGCTTTGCCACCTGAGGGA	2385
Qy	2563	GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA	2619
Db	2386	GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCTGTTA	2445

Qy	2620	TCTAATGACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTT	2679
Db	2446	CCTGATGAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTC	2505
Qy	2680	AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA	2739
Db	2506	AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA	2565
Qy	2740	AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTC	2799
Db	2566	ACTGAAACGTTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATC	2625
Qy	2800	AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC	2856
Db	2626	AGTTCTAAACTGATTCATTTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC	2685
Qy	2857	GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTG	2916
Db	2686	CACAAAAGTGAAATTGCTAATGCCCGGATGGAGCTGGGTCATTGCCTTGCCACAGAATTG	2745
Qy	2917	CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA	2970
Db	2746	CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA	2805
Qy	2971	GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC	3030
Db	2806	GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT	2865
Qy	3031	TCTGCTTTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA	3090
Db	2866	TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA	2925
Qy	3091	GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTCAGCTGTA	3150
Db	2926	GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA	2985
Qy	3151	TTGTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG	3210
Db	2986	TTTTCAGCAGAGCTGAGTAAAACCTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG	3045
Qy	3211	AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTGAGC	3270
Db	3046	AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTTATTGACAGTATTGAGC	3105
Qy	3271	ATTGTGAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG	3330
Db	3106	ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG	3165
Qy	3331	ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3390
Db	3166	ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA	3225
Qy	3391	TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTGAGAAATACAGTAATTCTGCT	3450
Db	3226	TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTGAGAAATACAGTAATTCTGCT	3285
Qy	3451	CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA	3510

Qy 433 CCCGCAGCCGGGCTGTCCGCAGCTGCGGTGC-----CGCCCGCCGCCGCCGCCGCGCTG 486
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 Db 175 CCCGCCCGCCGGGCTGTCCGCGGCCCCAGTGCCACCGCCCTGCCGCCGGCGCGCCCTG 234

Qy 487 CTGGACTTCAGCAGCGACTCGGTGCCCCCGCGCCCCGCGGGCCGCTGCCGGCCGCGCCC 546
 ||||| || | |||| ||||| || ||||| || || ||||| ||||| |||
 Db 235 ATGGACTTCGGAATGACTTCGTGCCGCCGGCGCCCCGGGGACCCCTGCCGGCCGCTCCC 294

Qy 547 CCTGCCGCTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCG-----CGGCGCCC 597
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 Db 295 CCCGTCGCCCCGAGCGGCAGCCGTCTTGGGACCCGAGCCCGGTGTGCTCGACCGTGCCC 354

Qy 598 GCGCCATCCCTGCCGCCCGCTGCCGCAGTCTGCCCTCCAAGCTCCCAGAGGACGACGAG 657
 ||||| || | | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 355 GCGCCATCCCGCTGTCTGTGCCGCAGTCTCGCCCTCCAAGCTCCCTGAGGACGACGAG 414

Qy 658 CCTCCGGCGAGGCCCCCGCTCCGCCGCCAGCCGGCGCGAGCCCCCTGGCGGAG----- 711
 ||||| ||||| || ||||| || || || || ||||| || || |||||
 Db 415 CCTCCGGCCCGGCTCCCCCTCCTCCCCCGCCAGCGTGAGCCCCCAGGCAGAGCCCGTG 474

Qy 712 -----CCCGCCGCGCCCCCTTCCACGCCGGCCGCGCCCAAGCGC 750
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 Db 475 TGGACCCCGCCAGCCCCGGCTCCCGCCGCGCCCCCTCCACCCGCGCGCCCAAGCGC 534

Qy 751 AGGGGCTCC---GGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 807
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 535 AGGGGCTCCTCGGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTGCTGCATCTGAGCCT 594

Qy 808 GTGATACCCTCCTCTGCAGAAAAAATTATGGATTTGATGGAGCAGCCAGGTAACACTGTT 867
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 595 GTGATACGCTCCTCTGCAGAAAA---TATGGACTTGAAGGAGCAGCCAGGTAACACTATT 651

Qy 868 TCGTCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCCTCTCTTCCTTCT 927
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 Db 652 TCGGCTGGTCAAGAGGATTTCCCATCTGTCTGCTTGAAACTGCTGCTTCTCTTCCTTCT 711

Qy 928 CTATCTCCTCTCTCAACTGTTTCTTTTAAAGAACATGGATACCTTGGTAACCTTATCAGCA 987
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 Db 712 CTGTCTCCTCTCTCAGCCGCTTCTTCAAAGAACATGAATACCTTGGTAATTTGTCAACA 771

Qy 988 GTGTATCCTCAGAAGGAACAATTGAAGAACTTTAAATGAAGCTTCTAAAGAGTTGCCA 1047
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 Db 772 GTATTACCCACTGAAGGAACACTTCAAGAAAATGTCAGTGAAGCTTCTAAAGAGGTCTCA 831

Qy 1048 GAGAGGGCAACAAATCCATTTGTAAATAGAGATTTAGCAGAATTTTCAGAATTAGAATAT 1107
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 Db 832 GAGAAGGCAAAACTCTACTCATAGATAGAGATTTAACAGAGTTTTCAGAATTAGAATAC 891

Qy 1108 TCAGAAATGGGATCATCTTTTAAAGGCTCCCCAAAAGGAGAGTCAGCCATATTAGTAGAA 1167
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 Db 892 TCAGAAATGGGATCATCGTTCAGTGTCTCTCCAAAAGCAGAATCTGCCGTAATAGTAGCA 951

Qy 1168 AACACTAAGGAAGAAGTAATTGTGAGGAGTAAA---GACAAAGAGGATTTAGTTTGTAGT 1224
 || |||| ||||| |||| |||| | |||| || |||| | ||||| |||||
 Db 952 AATCCTAGGAAGAAATAATCGTGAAAAATAAGATGAAGAAGAGAAGTTAGTTAGTAAT 1011

Qy 1225 GCAGCCCTTCACAGTCCACAAGAATCACCT-----GTGGGTAAAGAAGAC 1269

Db	1012	AACATCCTTCATAATCAACAAGAGTTACCTACAGCTCTTACTAAATTGGTTAAAGAGGAT	1071
Qy	1270	AGAGTTGTGTCTCCAGAAAAGACAATGGACATTTTAAATGAAATGCAGATGTCAGTAGTA	1329
Db	1072	GAAGTTGTGTCTTCAGAAAAGCAAAGACAGTTTAAATGAAAAGAGAGTTGCAGTGGAA	1131
Qy	1330	GCACCTGTGAGGGAAGAGTATGCAGACTTTAAGCCATTTGAACAAGCATGGGAAGTGAAA	1389
Db	1132	GCTCCTATGAGGGAGGAATATGCAGACTTCAAACCATTTGAGCGAGTATGGGAAGTGAAA	1191
Qy	1390	GATACTTATGAGGGAAGTAGGGATGTGCTGGCTGCTAGAGCT-----AATGTG	1437
Db	1192	GATA---GTAAGGAAGATAGTGATATGTTGGCTGCTGGAGGTAAAATCGAGAGCAACTTG	1248
Qy	1438	GAAAGTAAAGTGGACAGAAAATGCTTGGAGATAGCCTGGAGCAAAAAGTCTTGGGAAG	1497
Db	1249	GAAAGTAAAGTGGATAAAAAATGTTTGCAGATAGCCTTGAGCAAACTAATCACGAAAAA	1308
Qy	1498	GATAGTGAAGGCAGAAAATGAGGATGCTTCTTTCCCCAGTACCCAGAACCTGTGAAGGAC	1557
Db	1309	GATAGTGAGAGTAGTAATGATGATACTTCTTTCCCCAGTACGCCAGAAGGTATAAAGGAT	1368
Qy	1558	AGCTCCAGAGCATATATTACCTGTGCTTCCTTTACCT---CAGCAACCGAAAGCACCACA	1614
Db	1369	CGTCCAGGAGCATATATCACATGTGCTCCCTTTAACCAGCAGCAACTGAGAGCATTGCA	1428
Qy	1615	GCAAACACTTTCCCTTTGTTAGAAGATCATACTTCAGAAAATAAAACAGATGAAAAAAAA	1674
Db	1429	ACAAACATTTTTCCTTTGTTAGGAGATCCTACTTCAGAAAATAAGACCGATGAAAAAAAA	1488
Qy	1675	ATAGAAGAAAGGAAGGCCCAAATTATAACAGAGAAG---ACTAGCCCCAAAACGTCAAAT	1731
Db	1489	ATAGAAGAAAAGAAGGCCCAAATAGTAACAGAGAAGAATACTAGCACCAAACATCAAAC	1548
Qy	1732	CCTTTTCCTTGTTAGCAGTACAGGATTCTGAGGCAGATTATGTTACAACAGATACCTTATCA	1791
Db	1549	CCTTTTCCTTGTTAGCAGCACAGGATTCTGAGACAGATTATGTCACAACAGATAATTTAACA	1608
Qy	1792	AAGGTGACTGAGGCAGCAGTGTCAAACATGCCTGAAGGTCTGACGCCAGATTTAGTTCAG	1851
Db	1609	AAGGTGACTGAGGAAGTCGTGGCAAACATGCCTGAAGGCCTGACTCCAGATTTAGTACAG	1668
Qy	1852	GAAGCATGTGAAAGTGAAGTGAATGAAGCCACAGGTACAAAGATTGCTTATGAAACAAAA	1911
Db	1669	GAAGCATGTGAAAGTGAATTGAATGAAGTTACTGGTACAAAGATTGCTTATGAAACAAAA	1728
Qy	1912	GTGGACTTGGTCCAAACATCAGAAGCTATACAAGAATCACTTTACCCACAGCACAGCTT	1971
Db	1729	ATGGACTTGGTTCAAACATCAGAAGTTATGCAAGAGTCACTCTATCCTGCAGCACAGCTT	1788
Qy	1972	TGCCCATCATTTGAGGAAGCTGAAGCAACTCCGTCACCAGTTTTGCCTGATATTGTTATG	2031
Db	1789	TGCCCATCATTTGAAGAGTCAGAAGCTACTCCTTCACCAGTTTTGCCTGACATTGTTATG	1848
Qy	2032	GAAGCACCATTAAATTCTCTCCTTCCAAGCGCTGGTGCTTCTGTAGTGCAGCCAGTGTA	2091

Db 1849 GAAGCACCATTGAATTCTGCAGTTCCTAGTGCTGGTGCTTCCGTGATACAGCCCAGCTCA 1908
 Qy 2092 TCCCCACTGGAAGCACCTCCTCCAGTTAGTTATGACAGTATAAAGCTTGAGCCTGAAAAC 2151
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 Db 1909 TCACCATTAGAAG---CTTCTTCAGTTAATTATGAAAGCATAAAACATGAGCCTGAAAAC 1965
 Qy 2152 CCCCCACCATATGAAGAAGCCATGAATGTAGCACT---AAAAGCTTTGGGAACAAAGGAA 2208
 ||||| ||||| ||||| ||||| ||||| | ||||| |||||
 Db 1966 CCCCCACCATATGAAGAGGCCATGAGTGTATCACTAAAAAAGTATCAGGAATAAAGGAA 2025
 Qy 2209 GGAATAAAAGAGCCTGAAAGTTTTAATGCAGCTGTTCAAGAAACAGAAGCTCCTTATATA 2268
 | ||| ||||| ||||| | ||||| ||||| ||||| ||||| ||||| |||||
 Db 2026 GAAATTAAAGAGCCTGAAAATATTAATGCAGCTCTTCAAGAAACAGAAGCTCCTTATATA 2085
 Qy 2269 TCCATTGCGTGTGATTTAATTAAAGAAACAAAGCTCTCCACTGAGCCAAGTCCAGATTTT 2328
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 Db 2086 TCTATTGCATGTGATTTAATTAAAGAAACAAAGCTTTCTGCTGAACCAGCTCCGGATTTT 2145
 Qy 2329 TCTAATTATTCAGAAATAGCAAAATTCGAGAAGTCGGTGCCCGAACACGCTGAGCTAGTG 2388
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 Db 2146 TCTGATTATTCAGAAATGGCAAAAGTTGAACAGCCAGTGCCTGATCATTCTGAGCTAGTT 2205
 Qy 2389 GAGGATTCCTCACCTGAATCTGAACCAGTTGACTTATTTAGTGATGATTGCTGATTTCCTGAA 2448
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 Db 2206 GAAGATTCCTCACCTGATTCTGAACCAGTTGACTTATTTAGTGATGATTCAATACCTGAC 2265
 Qy 2449 GTCCACAAACACAAGAGGAGGCTGTGATGCTCATGAAGGAGAGTCTCACTGA-----A 2502
 || ||||| ||||| || ||||| ||||| ||||| || ||||| |||||
 Db 2266 GTTCCACAAAAACAAGATGAAACTGTGATGCTTGTGAAAGAAAGTCTCACTGAGACTTCA 2325
 Qy 2503 GTGTCTGAGACAGTAGCCCAGCACAAAGAGGAGAGACTTAGTGCCTCACCTCAGGAGCTA 2562
 | | ||| | ||| ||||| ||||| ||||| ||||| |||||
 Db 2326 TTTGAGTCAATGATAGAATATGAAAATAAGGAAAAACTCAGTGCTTTGCCACCTGAGGGA 2385
 Qy 2563 GGAAAGCCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCA 2619
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 Db 2386 GGAAAGCCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATAACCCTGTTA 2445
 Qy 2620 TCTAATGACATTCCAACATTGACCAAAAGGAGAAAAATTTCTTTGCAAATGGAAGAGTTT 2679
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 Db 2446 CCTGATGAAGTTTCAACATTGAGCAAAAGGAGAAAAATTCCTTTGCAGATGGAGGAGCTC 2505
 Qy 2680 AATACTGCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAA 2739
 | ||||| ||||| ||||| ||||| || ||||| ||||| ||||| |||||
 Db 2506 AGTACTGCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAA 2565
 Qy 2740 AGTGAAACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTG 2799
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 Db 2566 ACTGAAACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCTACATTGATC 2625
 Qy 2800 AGTGCTAAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCC 2856
 ||| |||| ||||| | ||||| ||||| || ||||| ||||| |||||
 Db 2626 AGTTCTAAACTGATTCAATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCC 2685
 Qy 2857 GACAAAAGTGAAATTGCTAATATCCAAAGCGGGGAGATTTCATTGCCTTGCTTAGAATTG 2916
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 Db 2686 CACAAAAGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTTCATTGCCTTGACACAGAATTG 2745

Qy 2917 CCCTGTGACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCA 2970
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 Db 2746 CCCCATGACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCA 2805
 Qy 2971 GATGAATTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTC 3030
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 Db 2806 GATGACTTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTT 2865
 Qy 3031 TCTGCTTTGGAACCTCAGACAGAAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAA 3090
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 Db 2866 TCTGCTTTGGCCACTCAAGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAA 2925
 Qy 3091 GAAGCAGAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGAGCTGTA 3150
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 Db 2926 GAAGCTGAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATA 2985
 Qy 3151 TTGTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAG 3210
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 Db 2986 TTTTCAGCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAG 3045
 Qy 3211 AAGACTGGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGC 3270
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 Db 3046 AAGACTGGAGTGGTGTGTTGGTGCCAGCCTATTCCTGCTGCTTTCATTGACAGTATTCAGC 3105
 Qy 3271 ATGTCAGTGTAAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGG 3330
 ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3106 ATTGTGAGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGG 3165
 Qy 3331 ATATATAAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA 3390
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 Db 3166 ATATACAAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCA 3225
 Qy 3391 TATTTAGAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCT 3450
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 Db 3226 TATCTGGAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAAGTACAGTAATTCTGCT 3285
 Qy 3451 CTTGGTCATGTGAACAGCACATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTA 3510
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3286 CTTGGTCATGTGAACTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTA 3345
 Qy 3511 GTTGATTCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTT 3570
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3346 GTTGATTCTCTGAAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTT 3405
 Qy 3571 AATGGTCTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTAT 3630
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3406 AATGGTCTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTTCTGTTATTTAT 3465
 Qy 3631 GAACGGCATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGAT 3690
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3466 GAACGGCATCAGGCGCAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGAT 3525
 Qy 3691 GCCATGGCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
 || ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 3526 GCTATGGCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 3575

Qy 2569 CCATATTTAGAGTCTTTTCAGCCCAATTTACATAGTACAAAAGATGC---TGCATCTAAT 2625
 ||||| || ||||| || || ||||| || ||||| || |||||
 Db 388 CCATATTTGGAATCTTTTAAGCTCAGTTTAGATAACACAAAAGATACCCTGTTACCTGAT 447

Qy 2626 GACATTCCAACATTGACCAAAAAGGAGAAAATTTCTTTGCAAATGGAAGAGTTTAATACT 2685
 || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 448 GAAGTTTCAACATTGAGCAAAAAGGAGAAAATTCCTTTGCAGATGGAGGAGCTCAGTACT 507

Qy 2686 GCAATTTATTCAAATGATGACTTACTTTCTTCTAAGGAAGACAAAATAAAAGAAAGTGAA 2745
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 508 GCAGTTTATTCAAATGATGACTTATTTATTTCTAAGGAAGCACAGATAAGAGAAACTGAA 567

Qy 2746 ACATTTTCAGATTCATCTCCGATTGAGATAATAGATGAATTTCCACGTTTGTGCTGCT 2805
 || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 568 ACGTTTTCAGATTCATCTCCAATTGAAATTATAGATGAGTTCCCTACATTGATCAGTCCT 627

Qy 2806 AAAGATGATTC---TCCTAAATTAGCCAAGGAGTACACTGATCTAGAAGTATCCGACAAA 2862
 ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 628 AAAACTGATTCATTTCTAAATTAGCCAGGGAATATACTGACCTAGAAGTATCCACAAA 687

Qy 2863 AGTGAAATTGCTAATATCCAAAGCGGGGCAGATTCATTGCCTTGCTTAGAATTGCCCTGT 2922
 ||||| ||||| || ||||| ||||| ||||| ||||| ||||| |||||
 Db 688 AGTGAAATTGCTAATGCCCCGGATGGAGCTGGGTCATTGCCTTGACACAGAATTGCCCCAT 747

Qy 2923 GACCTTTCTTTCAAGAATATATATCCTAAAGATGAAG-----TACATGTTTCAGATGAA 2976
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 748 GACCTTTCTTTGAAGAACATACAACCCAAAGTTGAAGAGAAAATCAGTTTCTCAGATGAC 807

Qy 2977 TTCTCCGAAAATAGGTCCAGTGTATCTAAGGCATCCATATCGCCTTCAAATGTCTCTGCT 3036
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 Db 808 TTTTCTAAAAATGGGTCTGCTACATCAAAGGTGCTCTTATTGCCTCCAGATGTTTCTGCT 867

Qy 3037 TTGGAACCTCAGACAGAAATGGGCAGCATAGTTAAATCCAAATCACTTACGAAAGAAGCA 3096
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 Db 868 TTGGCCACTCAGGCAGAGATAGAGAGCATAGTTAAACCCAAAGTTCTTGTGAAAGAAGCT 927

Qy 3097 GAGAAAAAACTTCCTTCTGACACAGAGAAAGAGGACAGATCCCTGTGCTGCTATTGTCA 3156
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 928 GAGAAAAAACTTCCTTCCGATACAGAAAAAGAGGACAGATCACCATCTGCTATATTTTCA 987

Qy 3157 GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTCTACTGGAGAGACATTAAGAAGACT 3216
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 Db 988 GCAGAGCTGAGTAAAACTTCAGTTGTTGACCTCCTGTACTGGAGAGACATTAAGAAGACT 1047

Qy 3217 GGAGTGGTGTGTTGGTGCCAGCTTATTCCTGCTGCTGTCTCTGACAGTGTTCAGCATTGTC 3276
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1048 GGAGTGGTGTGTTGGTGCCAGCCTATTCAGCTGCTTTTCATTGACAGTATTGAGCATTGTC 1107

Qy 3277 AGTGTAACGGCCTACATTGCCTTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATAT 3336
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 Db 1108 AGCGTAACAGCCTACATTGCCTTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATAC 1167

Qy 3337 AAGGGCGTGATCCAGGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCATATTTA 3396
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1168 AAGGGTGTGATCCAAGCTATCCAGAAATCAGATGAAGGCCACCCATTGAGGGCATATCTG 1227

Qy 3397 GAATCTGAAGTTGCTATATCAGAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGT 3456

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Db      1228  ||||| GAATCTGAAGTTGCTATATCTGAGGAGTTGGTTCAGAAGTACAGTAATTCTGCTCTTGGT 1287
Qy      3457  CATGTGAACAGCACAAATAAAAGAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGAT 3516
Db      1288  ||||| CATGTGAAGTGCACGATAAAGGAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGAT 1347
Qy      3517  TCCCTGAAGTTTGCAGTGTTGATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGT 3576
Db      1348  ||||| TCTCTGGAGTTTGCAGTGTTGATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGT 1407
Qy      3577  CTGACACTACTGATTTTAGCTCTGATCTCACTCTTCAGTATTCCTGTTATTTATGAACGG 3636
Db      1408  ||||| CTGACACTACTGATTTTGGCTCTCATTTCACTCTTCAGTGTTCCTGTTATTTATGAACGG 1467
Qy      3637  CATCAGGTGCAGATAGATCATTATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATG 3696
Db      1468  ||||| CATCAGGCACAGATAGATCATTATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATG 1527
Qy      3697  GCCAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCAGA 3740
Db      1528  ||||| GCTAAAATCCAAGCAAAAATCCCTGGATTGAAGCGCAAAGCTGA 1571

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RESULT 13

US-10-205-194-165

; Sequence 165, Application US/10205194

; Publication No. US20030134301A1

; GENERAL INFORMATION:

; APPLICANT: Warner-Lambert Company

; APPLICANT: Lee, Kevin

; APPLICANT: Dixon, Alistair

; APPLICANT: Brooksbank, Robert

; APPLICANT: Pinnock, Robert

; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain

; FILE REFERENCE: WL-A-018201

; CURRENT APPLICATION NUMBER: US/10/205,194

; CURRENT FILING DATE: 5200-07-24

; PRIOR APPLICATION NUMBER: GB 0118354.0

; PRIOR FILING DATE: 2001-07-27

; NUMBER OF SEQ ID NOS: 177

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 165

; LENGTH: 2782

; TYPE: DNA

; ORGANISM: Rattus norvegicus

; FEATURE:

; OTHER INFORMATION: Foocen-m2 reticulon

US-10-205-194-165

Query Match 21.6%; Score 809.8; DB 15; Length 2782;

Best Local Similarity 99.8%; Pred. No. 1.5e-201;

Matches 811; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 14 GCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAG 73

Db 462 GCGGCGGCGGCGGCTGCAGCCTGGGACAGGGCGGGTGGCACATCTCGATCGCGAAGGCAG 521

Qy	74	CAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGG	133
Db	522	GAGAAGCAGTCTCATTGTTCCGGGAGCCGTCGCCTCTGCAGGTTCTTCGGCTCGGCTCGG	581
Qy	134	CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCCAACCCCCACAACCGCCCGCGACT	193
Db	582	CACGACTCGGCCTGCCTGGCCCCCTGCCAGTCTTGCCCCAACCCCCACAACCGCCCGCGACT	641
Qy	194	CTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA	253
Db	642	CTGAGGAGAAGCGGCCCTGCGGCGGCTGTAGCTGCAGCATCGTCGGCGACCCGCCAGCCA	701
Qy	254	TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCTC	313
Db	702	TGGAAGACATAGACCAGTCGTCGCTGGTCTCCTCGTCCACGGACAGCCCGCCCCGGCCTC	761
Qy	314	CGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG	373
Db	762	CGCCCGCCTTCAAGTACCAGTTCGTGACGGAGCCCGAGGACGAGGAGGACGAGGAGGAGG	821
Qy	374	AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC	433
Db	822	AGGAGGACGAGGAGGAGGACGACGAGGACCTAGAGGAACTGGAGGTGCTGGAGAGGAAGC	881
Qy	434	CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCCGCCGCGCTGCTGGACT	493
Db	882	CCGCAGCCGGGCTGTCCGCAGCTGCGGTGCCGCCCGCCGCCCGCCGCGCTGCTGGACT	941
Qy	494	TCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCCCCTGCCG	553
Db	942	TCAGCAGCGACTCGGTGCCCCCGCGCCCCCGGGCCGCTGCCGGCCGCGCCCCCTGCCG	1001
Qy	554	CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCTGCCGC	613
Db	1002	CTCCTGAGAGGCAGCCATCCTGGGAACGCAGCCCCGCGGCGCCCGCGCCATCCTGCCGC	1061
Qy	614	CCGCTGCCGAGTCTTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC	673
Db	1062	CCGCTGCCGAGTCTTGCCCTCCAAGCTCCCAGAGGACGACGAGCCTCCGGCGAGGCCCC	1121
Qy	674	CGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC	733
Db	1122	CGCCTCCGCCGCCAGCCGGCGGAGCCCCCTGGCGGAGCCCGCCGCGCCCCCTTCCACGC	1181
Qy	734	CGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTG	793
Db	1182	CGGCCGCGCCCAAGCGCAGGGGCTCCGGCTCAGTGGATGAGACCCTTTTTGCTCTTCCTG	1241
Qy	794	CTGCATCTGAGCCTGTGATACCCTCCTCTGCAG	826
Db	1242	CTGCATCTGAACCTGTGATACCCTCCTCTGCAG	1274

RESULT 14

US-10-660-946-2

; Sequence 2, Application US/10660946

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; Publication No. US20040063131A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Au-Young, Janice
; Goli, Surya K.
; Hillman, Jennifer L.
; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/660,946
; FILING DATE: 12-Sep-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,213A
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/700,607
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 799 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: <Unknown>
; CLONE: Consensus
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-660-946-2

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Query Match          13.3%; Score 497.4; DB 13; Length 799;
Best Local Similarity 92.7%; Pred. No. 1e-119;
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
          |||
Db      108 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 167
          |||
Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTCAGTGTAACGGCCTACATTGCC 3297

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; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-789-386-5

Query Match 13.3%; Score 497.4; DB 9; Length 1122;
Best Local Similarity 92.7%; Pred. No. 1.3e-119;
Matches 522; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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Qy      3178 GTTGTGACCTCCTCTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 3237
          |||
Db      556 GTTGTGACCTCCTGTACTGGAGAGACATTAAGAAGACTGGAGTGGTGTGTTGGTGCCAGC 615

Qy      3238 TTATTCCTGCTGCTGTCTCTGACAGTGTTTCAGCATTGTTCAGTGTAAACGGCCTACATTGCC 3297
          |||
Db      616 CTATTCCTGCTGCTTTCATTGACAGTATTTCAGCATTGTGAGCGTAACAGCCTACATTGCC 675

Qy      3298 TTGGCCCTGCTCTCGGTGACTATCAGCTTTAGGATATATAAGGGCGTGATCCAGGCTATC 3357
          |||
Db      676 TTGGCCCTGCTCTCTGTGACCATCAGCTTTAGGATATACAAGGGTGTGATCCAAGCTATC 735

Qy      3358 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATTTAGAATCTGAAGTTGCTATATCA 3417
          |||
Db      736 CAGAAATCAGATGAAGGCCACCCATTCAGGGCATATCTGGAATCTGAAGTTGCTATATCT 795

Qy      3418 GAGGAATTGGTTCAGAAATACAGTAATTCTGCTCTTGGTCATGTGAACAGCACAATAAAA 3477
          |||
Db      796 GAGGAGTTGGTTCAGAAAGTACAGTAATTCTGCTCTTGGTCATGTGAACTGCACGATAAAG 855

Qy      3478 GAACTGAGGCGGCTTTTCTTAGTTGATGATTTAGTTGATTCCCTGAAGTTTGCAGTGTTG 3537
          |||
Db      856 GAACTCAGGCGCCTCTTCTTAGTTGATGATTTAGTTGATTCTCTGAAGTTTGCAGTGTTG 915

Qy      3538 ATGTGGGTGTTTACTTATGTTGGTGCCTTGTTCAATGGTCTGACACTACTGATTTTAGCT 3597
          |||
Db      916 ATGTGGGTATTTACCTATGTTGGTGCCTTGTTTAATGGTCTGACACTACTGATTTTGGCT 975

Qy      3598 CTGATCTCACTCTTCAGTATTCTGTTATTTATGAACGGCATCAGGTGCAGATAGATCAT 3657
          ||
Db      976 CTCATTTCACTCTTCAGTGTTCTGTTATTTATGAACGGCATCAGGCACAGATAGATCAT 1035

Qy      3658 TATCTAGGACTTGCAAACAAGAGTGTTAAGGATGCCATGGCCAAAATCCAAGCAAAAATC 3717
          |||
Db      1036 TATCTAGGACTTGCAAATAAGAATGTTAAAGATGCTATGGCTAAAATCCAAGCAAAAATC 1095

Qy      3718 CCTGGATTGAAGCGCAAAGCAGA 3740
          |||
Db      1096 CCTGGATTGAAGCGCAAAGCTGA 1118
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Job time : 1604.94 secs